BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

Amendments to the Specification:

At page 13, lines 16-30, please replace paragraph with the following:

The Expect value is used as a convenient way to create a significance threshold for reporting results. The default value used for blasting is typically set to 0.0001. In BLAST 2.0, the Expect value is also used instead of the P value (probability) to report the significance of matches. For example, an E value of one assigned to a hit can be interpreted as meaning that in a database of the current size one might expect to see one match with a similar score simply by chance. An E value of zero means that one would not expect to see any matches with a similar score simply by chance. ~~See, e.g., http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/.~~ Occasionally, a string of X's or N's will result from a BLAST search. This is a result of automatic filtering of the query for low-complexity sequence that is performed to prevent artifactual hits. The filter substitutes any low-complexity sequence that it finds with the letter "N" in nucleotide sequence (e.g., "NNNNNNNNNNNNN") or the letter "X" in protein sequences (e.g., "XXXXXXXXX"). Low-complexity regions can result in high scores that reflect compositional bias rather than significant position-by-position alignment. (Wootton and Federhen, Methods Enzymol 266:554-571, 1996) ~~(Wootton and Federhen, Methods Enzymol 266:554-571, 1996)~~.

At page 23, please replace Table 1J with the following:

Table 1J. BLAST results for NOV1a

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
~~gi|13569928|ref|NP_112217.1|~~ NP 112217	a disintegrin-like and metalloprotease with thrombospondin type 1 motif, 12 [Homo sapiens]	1593	269/616 (43%)	371/616 (59%)	e-135
~~gi|11493589|gb|AAG35563.1|AF163762_1 (AF163762)~~ AAG35563	zinc metalloendopeptidase [Homo sapiens]	1077	253/624 (40%)	359/624 (56%)	e-128

~~gi|10645199|ref|NP_055087.1|~~ NP_055087	a disintegrin and metalloprotease with thrombospondin motifs-7 preproprotein; a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 7 [Homo sapiens]	997	247/571 (43%)	344/571 (59%)	e-127
~~gi|15309931|ref|XP_054419.1|~~ XP_054419	a disintegrin-like and metalloprotease domain with thrombospondin type I repeats 10 [Homo sapiens]	854	245/604 (40%)	348/604 (57%)	e-124
~~gi|7656869|ref|NP_055088.1|~~ NP_055088	a disintegrin and metalloprotease with thrombospondin motifs-6 preproprotein; a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 6 [Homo sapiens]	860	244/630 (38%)	345/630 (54%)	e-115

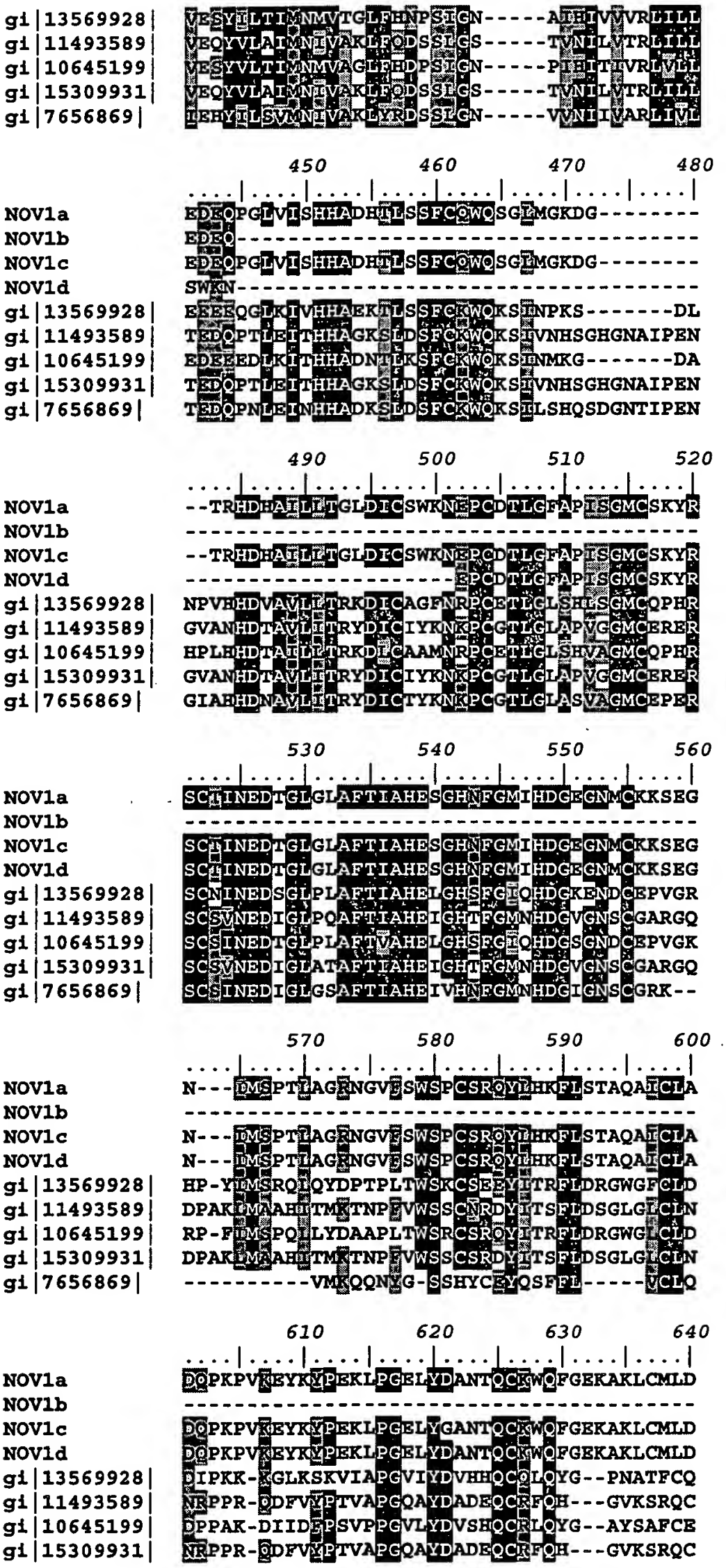
At page 24 please replace Table 1K with the following:

Table 1K. ClustalW Analysis of NOV1

1) Novel NOV1a (SEQ ID NO:2)
2) Novel NOV1b (SEQ ID NO:4)
3) Novel NOV1c (SEQ ID NO:6)
4) Novel NOV1d (SEQ ID NO:8)
4) ~~gi\|13569928\|ref\|NP_112217.1\|~~ **gi\|13569928\|** NP_112217 a disintegrin-like and metalloprotease with thrombospondin type 1 motif, 12 [Homo sapiens] (SEQ ID NO:30)
5) ~~gi\|11493589\|gb\|AAG35563.1\|AF163762_1~~ **gi\|11493589\|** AAG35563 (AF163762) zinc metalloendopeptidase [Homo sapiens] (SEQ ID NO:31)
6) ~~gi\|10645199\|ref\|NP_055087.1\|~~ **gi\|10645199\|** NP_055087 a disintegrin and metalloprotease with thrombospondin motifs-7 preproprotein; a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 7 [Homo sapiens] (SEQ ID NO:32)
7) ~~gi\|15309931\|ref\|XP_054419.1\|~~ **gi\|15309931\|** XP_054419 a disintegrin-like and metalloprotease domain with thrombospondin type I repeats 10 [Homo sapiens] (SEQ ID NO:33)
8) ~~gi\|7656869\|ref\|NP_055088.1\|~~ **gi\|7656869\|** NP_055088 a disintegrin and metalloprotease with thrombospondin motifs-6 preproprotein; a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 6 [Homo sapiens] (SEQ ID NO:34)

```
                    10        20        30        40
                    ....|....|....|....|....|....|....|....|
NOV1a               MKPRARGWRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQ
NOV1b               MKPRARGWRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQ
NOV1c               ----------------------------------------
NOV1d               MKPRARGWRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQ
gi|13569928|        ----------------------------------------
gi|11493589|        ----------------------------------------
gi|10645199|        ----------------------------------------
gi|15309931|        ----------------------------------------
gi|7656869|         ----------------------------------------

                    50        60        70        80
                    ....|....|....|....|....|....|....|....|
NOV1a               LEASPPRLLSRGPRRLTAMSPLFSAGTCVRHGTRSGSAWE
NOV1b               LEASPPRLLSRGPRRLTAMSPLFSAGTCVRHGTRSGSAWE
NOV1c               ----------MGP---AAAAP--------------GSPSV
NOV1d               LEASPPRLLSRGPRRLTAMSPLFSAGTCVRHGTRSGSAWE
gi|13569928|        ---MPCAQRSWLANLSVVAQLLNFGALCYGRQPQPGPVRF
gi|11493589|        ----------------------------------------
gi|10645199|        ---MPGGPSPRSPAPLLRPLLLLLCALAPG-APGPAPGRA
gi|15309931|        ----------------------------------------
gi|7656869|         ------------MEILWKTLTWILSLIMASSEFHSDHRL

                    90        100       110       120
                    ....|....|....|....|....|....|....|....|
NOV1a               PERPASSSTRGAAGLDGKGRDMDEAGNHRSQQTNTGTENQ
NOV1b               PERPASSSTRGAAGLDGKGRDMDEAGNHRSQQTNTGTENQ
NOV1c               PRPPP-----------------------------------
NOV1d               PERPASSSTRGAAGLDGKGRDMDEAGNHRSQQTNTGTENQ
gi|13569928|        PDRRQEHFIKGL----------------------------
gi|11493589|        --RSQDEFLSSL----------------------------
gi|10645199|        TEGR------------------------------------
gi|15309931|        ----------------------------------------
gi|7656869|         SYSSQEEFLTYL----------------------------

                    130       140       150       160
                    ....|....|....|....|....|....|....|....|
NOV1a               TLHVLT-QYDLVSAYEVDHRGDYVSHELMHHQR-RRRAVA
NOV1b               TLHVLTREYDLVSAYEVDHRGDYVSHELMHHQR-RRRAVA
NOV1c               ---------DLVSAYEVDHRGDYVSHELMHHQR-RRRAVA
NOV1d               TLHVLT-QYDLVSAYEVDHRGDYVSHELMHHQR-RRRAVA
gi|13569928|        ------PEYHVVGPVRVDASGHFLSYGLHYPITSSRRKRD
gi|11493589|        ------ESYELAFPTRVDHNGALLAFSPPPP-RRQRRGTG
gi|10645199|        ------AALDIVHPVRVDAGGSFLSYELWP--R-ALRKRD
gi|15309931|        ----------------------------------------
gi|7656869|         ------EHYQLTIPIRVDQNGAFLSFTVKND-KHSRRRRS

                    170       180       190       200
                    ....|....|....|....|....|....|....|....|
NOV1a               VS-----EVES-LHLRIKGPRHDFHMDLRTSSSLVAPGFI
NOV1b               VS-----EVES-LHLRIKGPRHDFHMDLRTSSSLVAPGFI
NOV1c               VS-----EVEP-AFLQVCRARELRLCVEAFPIANSQPGFL
NOV1d               VS-----EVES-LHLRIKGPRHDFHMDLRTSSSLVAPGFI
gi|13569928|        ID----GSEDW-VYYRISHEEKDLFFNLTVNQGFLSNSYI
gi|11493589|        AT------AESRLFYKVASPSTHFLLNLTRSSRLLAGHVS
gi|10645199|        VS----VRRDAPAFYELQYRGRELRFNLTANQHLLAPGFV
gi|15309931|        ----------------------------------------
gi|7656869|         MDPIDPQQAVSKLFFKISAYGKHFHLNLTLNTDFVSKHFT

                    210       220       230       240
                    ....|....|....|....|....|....|....|....|
```

```
NOV1a          VQTLGKTGTKSVQTLP--P-EDFCFYQGSLRSHRNSPSHG
NOV1b          VQTLGKTGTKSVQTLP--P-EDFCFYQGSLRSHRNSPSHG
NOV1c          NLSNVKSHWREQHASKRII-TNAMLGESALASTRKS---N
NOV1d          VQTLGKTGTKSVQTLP--P-EDFCFYQGSLRSHRNSPSHG
gi|13569928|   MEKR-YGNLSHVKMMAS--SAPLCHLSGTVLQQGTRVGTA
gi|11493589|   VEYWTREGLAWQRAARP-----HCLYAGHLQGQASSS-HV
gi|10645199|   SETRRRGGLGRAHIRAH---TPACHLLGEVQDPELEGGLA
gi|15309931|   ----------------------------------------
gi|7656869|    VEYWGKDGPQWKHDFLD-----NCHYTGYLQDQRSTT-KV

                         250       260       270       280
               ....|....|....|....|....|....|....|....|
NOV1a          GKFCEGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFR
NOV1b          GKFCEGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFR
NOV1c          CVFFL-S---FYFFQSGMIRTEEADYFLRPLPSHLSWKLG
NOV1d          GKFCEGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFR
gi|13569928|   ALSACHG-------LTGFFQLPHGDEFIEPVKKHPLVEG-
gi|11493589|   AISTCGG-------LHGLIVADEEEYLIEPLHGGPKGS--
gi|10645199|   AISACDG-------LKGVFQLSNEDYFIEPLDSAPARPG-
gi|15309931|   ----------------------------------------
gi|7656869|    ALSNCVG-------LHGVIATEDEEYFIEPLKNTTEDSKH

                         290       300       310       320
               ....|....|....|....|....|....|....|....|
NOV1a          GRHYKWKPYTQVEXDLCKLYCIAEGFDFFFSLSNKVKDGT
NOV1b          GRHYKWKPYTQVEQDLCKLYCIAEGFDFFFSLSNKVKDGT
NOV1c          RAAQGSSPSHVLYKREVLVTSRTWELAHQPLHSSDLRLGL
NOV1d          GRHYKWKPYTQVEADLCKLYCIAEGFDFFFSLSNKVKDGT
gi|13569928|   ----GYHPHIVYRRQKVP--------ETKEP-TCGLKDSV
gi|11493589|   RSPEESGPHVVYKRSSLRHPHLDTACGV-RDEKPWKGRPW
gi|10645199|   ----HAQPHVVYKRQAPER--LAQRGDSSAPSTCGVQVYP
gi|15309931|   ----------------------------------------
gi|7656869|    FSYENGHPHVIYKKSALQQRHLYDHSHCGVSDFTRSGKPW

                         330       340       350       360
               ....|....|....|....|....|....|....|....|
NOV1a          PCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDE
NOV1b          PCSEDSRNVCIDGICE---------MPQPPKEDLFILPDE
NOV1c          PQKQHFCGRRKK------------YMPQPPKEDLFILPDE
NOV1d          PCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDE
gi|13569928|   NISQ----------------------------KQELWREK
gi|11493589|   WLRT----------------------------LKPPPARP
gi|10645199|   ELES----------------------------RRERWEQR
gi|15309931|   ----------------------------------------
gi|7656869|    WLN-----------------------------DTSTVSYS

                         370       380       390       400
               ....|....|....|....|....|....|....|....|
NOV1a          YKSCLRHKRSLLRSHRNEELNVETLVVVDKKMMQNHGHEN
NOV1b          YKSCLRHKRSLLRSHRNEELNVETLVVVDKKMMQNHGHEN
NOV1c          YKSCLRHKRSLLRSHRNEELNVETLVVVDKKMMQNHGHEN
NOV1d          YKSCLRHKRSLLRSHRNEELNVETLVVVDKKMMQNHGHEN
gi|13569928|   WERHNLPSRSLSRRSISKERWVETLVVADTKMIEYHGSEN
gi|11493589|   LGNETERGQPGLKRSVSRERYVETLVVADKMMVAYHGRRD
gi|10645199|   QQWRRPRLRRLHQRSVSKEKWVETLVVADAKMVEYHGQPQ
gi|15309931|   ------------------------------MMVAYHGRRD
gi|7656869|    LPINNTHIHHRQKRSVSIERFVETLVVADKMMVGYHGRKD

                         410       420       430       440
               ....|....|....|....|....|....|....|....|
NOV1a          ITTYVLTILNMVSALFKDGTIGG-----NINIAIVGLILL
NOV1b          ITTYVLTILNMVSALFKDGTIGG-----NINIAIVGLILL
NOV1c          ITTYVLTILNMVSALFKDGTIGG-----NINIAIVGLILL
NOV1d          ITTYVLTILNMVSALFKDGLMGKDGTRHDHAILLTGLDIC
```


gi|13569928|
gi|11493589|
gi|10645199|
gi|15309931|
gi|7656869|
450 460 470 480
NOV1a
NOV1b
NOV1c
NOV1d
gi|13569928|
gi|11493589|
gi|10645199|
gi|15309931|
gi|7656869|
490 500 510 520
NOV1a
NOV1b
NOV1c
NOV1d
gi|13569928|
gi|11493589|
gi|10645199|
gi|15309931|
gi|7656869|
530 540 550 560
NOV1a
NOV1b
NOV1c
NOV1d
gi|13569928|
gi|11493589|
gi|10645199|
gi|15309931|
gi|7656869|
570 580 590 600
NOV1a
NOV1b
NOV1c
NOV1d
gi|13569928|
gi|11493589|
gi|10645199|
gi|15309931|
gi|7656869|
610 620 630 640
NOV1a
NOV1b
NOV1c
NOV1d
gi|13569928|
gi|11493589|
gi|10645199|
gi|15309931|

```
gi|7656869|    SRX--------------------------------HHQ

                        650       660       670       680
                ....|....|....|....|....|....|....|....|
NOV1a           FKKDICKALWCHRIGRKCETKFMPAAEGTICG----HDMW
NOV1b           ---DICKALWCHRIGRKCETKFMPAAEGTICG----HDMW
NOV1c           FKKDICKALWCHRIGRKCETKFMPAAEGTICG----HEHG
NOV1d           FKKDICKALWCHRIGRKCETKFMPAAEGTICG----HDMW
gi|13569928|    EVENVCQTLWCSVKG-FCRSKLDAAADGTQCG----EKKW
gi|11493589|    KYGEVCSELWCLSKSNRCITNSIPAAEGTLCQTHTIDKGW
gi|10645199|    DMDNVCHTLWCSVGT-TCHSKLDAAVDGTRCG----ENKW
gi|15309931|    KYGEVCSELWCLSKSNRCITNSIPAAEGTLCQTHTIDKGW
gi|7656869|     LFREVCRELWCLSKSNRCVTNSIPAAEGTICQTGNIEKGW

                        690       700       710       720
                ....|....|....|....|....|....|....|....|
NOV1a           CRGGQCVKYGDEGPKPTHGHWSDWSSWSPCSRTCGGGVSH
NOV1b           CRGGQCVKYGDEGPKPTHGHWSDWSSWSPCSRTCGGGVSH
NOV1c           A-GGQCVKYGDEGPKPTHGHWSDWSSWSPCSRTCGGGVSH
NOV1d           CRGGQCVKYGDEGPKPTHGHWSDWSSWSPCSRTCGGGVSH
gi|13569928|    CMAGKCITVGKK-PESIPGGWGRWSPWSHCSRTCGAGVQS
gi|11493589|    CYKRVCVPFGSR-PEGVDGAWGPWTPWGDCSRTCGGGVSS
gi|10645199|    CLSGECVPVGFR-PEAVDGGWSGWSAWSICSRSCGMGVQS
gi|15309931|    CYKRVCVPFGSR-PEGVDGAWGPWTPWGDCSRTCGGGVSS
gi|7656869|     CYQGDCVPFGTW-PQSIDGGWGPWSLWGECSRTCGGGVSS

                        730       740       750       760
                ....|....|....|....|....|....|....|....|
NOV1a           RSR-LCTNPNPSHGGKFCEGSTRTLKLCNSQKCPRDSVDF
NOV1b           RSR-LCTNPRPSHGGKFCEGSTRTLKLCNSQKCPRDSVDF
NOV1c           RSRSQNTHSRPSHGGKFCEGSTRTLKLCNSQKCPRDSVDF
NOV1d           RSR-LCTNPKPSHGGKFCEGSTRTLKLCNSQKCPRDSVDF
gi|13569928|    AER-LCNNPEPKFGGKYCTGERKRYRLCNVHPCRSEAPTF
gi|11493589|    SSR-HCDSPRPTIGGKYCLGERRRHRSCNTDDCPPGSQDF
gi|10645199|    AER-QCTQPTPKYKGRYCVGERKRFRLCNLQACPAGRPSF
gi|15309931|    SSR-HCDSPRPTIGGKYCLGERRRHRSCNTDDCPPGSQDF
gi|7656869|     SLR-HCDSPAPSGGGKYCLGERKRYRSCNTDPCPLGSRDF

                        770       780       790       800
                ....|....|....|....|....|....|....|....|
NOV1a           RAAQCAEHNSRRFRGRHYKWKP------QDLCKLYCIAEG
NOV1b           RAAQCAEHNSRRFRGRHYKWKP------QDLCKLYCIAEG
NOV1c           RAAQCAEHNSRRFRGRHYKWKP-----DQDLCKLYCIAEG
NOV1d           RAAQCAEHNSRRFRGRHYKWKPYTQVEDQDLCKLYCIAEG
gi|13569928|    RQMQCSEFDIVPYKNELYHWFPIFN--PAHPCELYCRPID
gi|11493589|    REVQCSEFDSIPFRGKFYKWKTYRGG-GVKACSLTSIAEG
gi|10645199|    RHVQCSHFDAMLYKGQLHTWVPVVN--DVNPCEEHCRPAN
gi|15309931|    REVQCSEFDSIPFRGKFYKWKTYRGG-GVKACSLTCIAEG
gi|7656869|     REKQCADFDNMPFRGKYYNWKPYTGG-GVKPCALNCLAEG

                        810       820       830       840
                ....|....|....|....|....|....|....|....|
NOV1a           FDFEFSLSNKVKDGTPCS--EDSRNVCIDGICEX-GCDNV
NOV1b           FDFEFSLSNKVKDGTPCS--EDSRNVCIDGICE--GCDNV
NOV1c           FDFEFSLSNKVKDGTPCS--EDSRNVCIDGICERVGCDNV
NOV1d           FDFEFSLSNKVKDGTPCS--EDSRNVCIDGICERVGCDNV
gi|13569928|    GQFSEKMLDAVIDGTPCFEGGNSRNVCINGICKMVGCDYE
gi|11493589|    FNFYTERAAAVVDGTPCR--PDTVDICVSGECKHVGCDRV
gi|10645199|    EYFAKKLRDAVVDGTPCYQVRASRDLCINGICKNVGCDFE
gi|15309931|    FNFYTERAAAVVDGTPCR--PDTVDICVSGECKHVGCDRV
gi|7656869|     YNFYTERAPAVIDGTQCN--ADSLDICINGECKHVGCDNI

                        850       860       870       880
                ....|....|....|....|....|....|....|....|
```

```
NOV1a         LGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTN-HYHMV
NOV1b         LGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTN-YYHMV
NOV1c         LGSDAVEDVCGVCNGNNSACTIHRGLY---LE---YYHMV
NOV1d         LGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTNQYYHMV
gi|13569928|  IDSNATEDRCGVCLGDGSSCQTVRKMFKQKE-GSGYVDIG
gi|11493589|  LGSDLREDKCRVCGGDGSACETIEGVFSPASPGAGYEDVV
gi|10645199|  IDSGAMEDRCGVCHGNGSTCHTVSGTFEEAE-GLGYVDVG
gi|15309931|  LGSDLREDKCRVCGGDGSACETIEGVFSPASPGAGYEDVV
gi|7656869|   LGSDAREDRCRVCGGGGSTCDAIEGFENDSLPRGGYMEVV

                      890       900       910       920
              ....|....|....|....|....|....|....|....|
NOV1a         TIPSGARSIRIYEMNVSTSYISVRN-ALRRYYLNGHWTVD
NOV1b         TIPSGARSIRIYEMNVSTSYISVRN-ALRRYYLNGHWTVD
NOV1c         TIPSGARSIRIYEMNVSTSYISVRN-ALRRYYLNGHWTVD
NOV1d         TIPSGARSIRIYEMNVSTSYISVRN-ALRRYYLNGHWTVD
gi|13569928|  LIPKGARDIRVMEIEGAGNFLAIRSEDPEKYYLNGGFIIQ
gi|11493589|  WIPKGSVHIFIQDLNLSLSHLALKGDQ-ESLLLEGLPGTP
gi|10645199|  LIPAGAREIRIQEVAEAANFLALRSEDPEKYFLNGGWTIQ
gi|15309931|  WIPKGSVHIFIQDLNLSLSHLALKGDQ-ESLLLEGLPGTP
gi|7656869|   QIPRGSVHIEVREVAMSKNYIALKSEG-DDYYINGAWTID

                      930       940       950       960
              ....|....|....|....|....|....|....|....|
NOV1a         WPGRYKFSGTTFDYRRSYNEPENLIATGPTNETLIVELLF
NOV1b         WPGRYKFSGTTFDYRRSYNEPENLIATGPTNETLIVELLF
NOV1c         WPGRYKFSGTTFDYRRSYNEPENLIATGPTNETLIVELLF
NOV1d         WPGRYKFSGTTFDYRRSYNEPENLIATGPTNETLIVELLF
gi|13569928|  WNGNYKLAGTVFQYDRKGD-LEKLMATGPTNESVWIQLLF
gi|11493589|  QPHRLPLAGTTFQLRQGPDQVQSLEALGPINASLIVMVLA
gi|10645199|  WNGDYQVAGTTFTYARRGN-WENLTSPGPTKEPVWIQ---
gi|15309931|  QPHRLPLAGTTFQLRQGPDQVQSLEALGPINASLIVMVLA
gi|7656869|   WPRKFDVAGTAFHYKRPTDEPESLEALGPTSENLIVMVLL

                      970       980       990      1000
              ....|....|....|....|....|....|....|....|
NOV1a         QGRNPGVAWEYS----------------------------
NOV1b         QGRNPGVAWEYS----------------------------
NOV1c         QGRNPGVAWEYS----------------------------
NOV1d         QGRNPGVAWEYS----------------------------
gi|13569928|  QVTNPGIKYEYTIQKDGLDNDVEQMYFWQYGHWTECSVTC
gi|11493589|  RTELPALRYRFN----------------------------
gi|10645199|  ----------------------------------------
gi|15309931|  RTELPALRYRFN----------------------------
gi|7656869|   QEQNLGIRYKFN----------------------------

                     1010      1020      1030      1040
              ....|....|....|....|....|....|....|....|
NOV1a         ----------------------------------------
NOV1b         ----------------------------------------
NOV1c         ----------------------------------------
NOV1d         ----------------------------------------
gi|13569928|  GTGIRRQTAHCIKKGRGMVKATFCDPETQPNGRQKKCHEK
gi|11493589|  -APIAR--------------------------------DS
gi|10645199|  ---VP-----------------------------------
gi|15309931|  -APIAR--------------------------------DS
gi|7656869|   -VPITRTGSG----------------------------DN

                     1050      1060      1070      1080
              ....|....|....|....|....|....|....|....|
NOV1a         --------------MPRLGTE-------------------
NOV1b         --------------MPRLGTE-------------------
NOV1c         --------------MPRLGTE-------------------
NOV1d         --------------MPRLGTE-------------------
```

```
gi|13569928|  ACPPRWWAGEWEACSATCGPHGEKKRTVLCIQTMVSDEQA
gi|11493589|  LPPYSWHYAPWTKCSAQCAGGSQV-QAVECRNQL--DSSA
gi|10645199|  ---------------ASRGPGGGS-R-----------GG
gi|15309931|  LPPYSWHYAPWTKCSAQCAGGSQV-QAVECRNQL--DSSA
gi|7656869|   EVGFTWNHQPWSECSATCAGG-----------------

                      1090      1100      1110      1120
                      ....|....|....|....|....|....|....|
NOV1a         ----------KQPPAQPS---------------------
NOV1b         ----------KQPPAQPS---------------------
NOV1c         ----------KQPPAQPS---------------------
NOV1d         ----------KQPPAQPS---------------------
gi|13569928|  LPPTDCQ-HLLKPKTLLSCNRDILCPSDWTVGNWSECSVS
gi|11493589|  VAPHYCSAHSKLPKRQRACNTEP-CPPDWVVGNWSLCSRS
gi|10645199|  VP---------RPSTLHGRSR---------------P---
gi|15309931|  VAPHYCSAHSKLPKRQRACNTEP-CPPDWVVGNWSLCSRS
gi|7656869|   ----------KMPTRQ-----P---------------TQR

                      1130      1140      1150      1160
                      ....|....|....|....|....|....|....|
NOV1a         -----YTWAIVR-----------------------------
NOV1b         -----YTWAIVR-----------------------------
NOV1c         -----YTWAIVR-----------------------------
NOV1d         -----YTWAIVR-----------------------------
gi|13569928|  CGGGVRIRSVTCAKNHDEPCDVTRKPNSRALCGLQQCPSS
gi|11493589|  CDAGVRSRSVVCQR-------------------------
gi|10645199|  --GGVSPGSVT------------E-PGS------------
gi|15309931|  CDAGVRSRSVVCQR-------------------------
gi|7656869|   --ARWRTKHTLSY-------------------------

                      1170      1180      1190      1200
                      ....|....|....|....|....|....|....|
NOV1a         ----------------------------------------
NOV1b         ----------------------------------------
NOV1c         ----------------------------------------
NOV1d         ----------------------------------------
gi|13569928|  RRVLKPNKGTISNGKNPPTLKPVPPPTSRPRMLTTPTGPE
gi|11493589|  --------------RVSAAEEKALDDSACPQ---------
gi|10645199|  --------------------EPGPPAAAS-----------
gi|15309931|  --------------RVSAAEEKALDDSACPQ---------
gi|7656869|   ---------------ALCLLKKLIGNISCR----------

                      1210      1220      1230      1240
                      ....|....|....|....|....|....|....|
NOV1a         --------------------------SECSVSCGGGRC
NOV1b         --------------------------SECSVSCGGGRC
NOV1c         --------------------------SECSVSCGGGRC
NOV1d         --------------------------SECSVSCGGGRC
gi|13569928|  SMSTSTPAISSPSPTTASKEGDLGGKQWQDS--STQPELS
gi|11493589|  ---PRPPVLEACHGPTCPPEW--AALDWSECTPSCGPGLR
gi|10645199|  -T-SVSPSLKWPNLVAAVHRG-----GWGQA--PLGLGGW
gi|15309931|  ---PRPPVLEACHGPTCPPEW--AALDWSECTPSCGPGLR
gi|7656869|   --------------------------FAS---SCN--LA

                      1250      1260      1270      1280
                      ....|....|....|....|....|....|....|
NOV1a         LPVLLLEAACQPSATAYIALAFLES---------------
NOV1b         LPVLLLEAACQPSATAYIALAFLES---------------
NOV1c         LPVLLLEAACQPLATAYIALAFLES---------------
NOV1d         LPVLLLEAACQPSATAYIALAFLES---------------
gi|13569928|  SRYLISTGSTSQPILTSQSLSIQPSEENVSSSDTGPTSEG
gi|11493589|  HRVVLCKSADHRATLPPAHCSPAAKP--------------
gi|10645199|  RRHLVLMG----PRLPTQLLFQE--------------SNP
gi|15309931|  HRVVLCKSADHRATLPPAHCSPAAKP--------------
```

```
gi|7656869|   KETLL----------------------------------

                        1290      1300      1310      1320
                ....|....|....|....|....|....|....|....|
NOV1a           ----------------------------------------
NOV1b           ----------------------------------------
NOV1c           ----------------------------------------
NOV1d           ----------------------------------------
gi|13569928|  GLVATTTSGSGLSSSRNPITWPVTPFYNTLTKGPEMEIHS
gi|11493589|  ----------------------------------------PAT
gi|10645199|  G-----------------VHYEYT-------------IHR
gi|15309931|  ----------------------------------------PAT
gi|7656869|   ----------------------------------------

                        1330      1340      1350      1360
                ....|....|....|....|....|....|....|....|
NOV1a           ----------------------------------------
NOV1b           ----------------------------------------
NOV1c           ----------------------------------------
NOV1d           ----------------------------------------
gi|13569928|  GSGEEREQPEDKDESNPVIWTKIRVPGNDAPVESTEMPLA
gi|11493589|  MRCNLRRCPP------------------------------
gi|10645199|  EAGGHDEVPP------------------------------
gi|15309931|  MRCNLRRCPP------------------------------
gi|7656869|   ----------------------------------------

                        1370      1380      1390      1400
                ....|....|....|....|....|....|....|....|
NOV1a           ----------------------------------------
NOV1b           ----------------------------------------
NOV1c           ----------------------------------------
NOV1d           ----------------------------------------
gi|13569928|  PPLTPDLSRESWWPPFSTVMEGLLPSQRPTTSETGTPRVE
gi|11493589|  ----------------------------------------
gi|10645199|  ----------------------------------------
gi|15309931|  ----------------------------------------
gi|7656869|   ----------------------------------------

                        1410      1420      1430      1440
                ....|....|....|....|....|....|....|....|
NOV1a           ----------------------------------------
NOV1b           ----------------------------------------
NOV1c           ----------------------------------------
NOV1d           ----------------------------------------
gi|13569928|  GMVTEKPANTLLPLGGDHQPEPSGKTANRNHLKLPNNMNQ
gi|11493589|  ----------------------------------------
gi|10645199|  ----------------------------------------
gi|15309931|  ----------------------------------------
gi|7656869|   ----------------------------------------

                        1450      1460      1470      1480
                ....|....|....|....|....|....|....|....|
NOV1a           ----------------------------------------
NOV1b           ----------------------------------------
NOV1c           ----------------------------------------
NOV1d           ----------------------------------------
gi|13569928|  TKSSEPVLTEEDATSLITEGFLLNASNYKQLTNGHGSAHW
gi|11493589|  ----------------------------------------ARW
gi|10645199|  -----PVFS--------------------------------W
gi|15309931|  ----------------------------------------ARW
gi|7656869|   ----------------------------------------

                        1490      1500      1510      1520
                ....|....|....|....|....|....|....|....|
```

```
NOV1a          ----------------------------------------
NOV1b          ----------------------------------------
NOV1c          ----------------------------------------
NOV1d          ----------------------------------------
gi|13569928|   IVGNWSECSTTCGLGAYWKRVECTTQMDSDCAAIQRPDPA
gi|11493589|   VAGEWGECSAQCGVGQRQRSVRCTS--------------
gi|10645199|   HYGPWTKCTVTCGRGE------------------------
gi|15309931|   VAGEWGECSAQCGVGQRQRSVRCTS--------------
gi|7656869|    ----------------------------------------

                       1530      1540      1550      1560
               ....|....|....|....|....|....|....|....|
NOV1a          ----------------------------------------
NOV1b          ----------------------------------------
NOV1c          ----------------------------------------
NOV1d          ----------------------------------------
gi|13569928|   KRCHLRPCAGWKVGNWSKCSRNCSGGFKIREIQCVDSRDH
gi|11493589|   --------------HTGQASHECTEALR------------
gi|10645199|   --------------KWGRHSPTCRG--------LVSGQGH
gi|15309931|   --------------HTGQASHECTEALR------------
gi|7656869|    ----------------------------------------

                       1570      1580      1590      1600
               ....|....|....|....|....|....|....|....|
NOV1a          ----------------------------------------
NOV1b          ----------------------------------------
NOV1c          ----------------------------------------
NOV1d          ----------------------------------------
gi|13569928|   RNLRPFHCQFLAGIPPPLSMSCNPEPCEAWQVEPWSQCSR
gi|11493589|   -------------------------------PPTTQQCEA
gi|10645199|   ---------------------------------WLQLPA
gi|15309931|   -------------------------------PPTTQQCEA
gi|7656869|    ----------------------------------------

                       1610      1620      1630      1640
               ....|....|....|....|....|....|....|....|
NOV1a          ----------------------------------------
NOV1b          ----------------------------------------
NOV1c          ----------------------------------------
NOV1d          ----------------------------------------
gi|13569928|   SCGGGVQERGVFCPGGLCDWTKRPTSTMSCNEHLCCHWAT
gi|11493589|   KCDS--------------------------------PTPG
gi|10645199|   HC----------------------------------WAT
gi|15309931|   KCDS--------------------------------PTPG
gi|7656869|    ----------------------------------------

                       1650      1660      1670      1680
               ....|....|....|....|....|....|....|....|
NOV1a          ----------------------------------------
NOV1b          ----------------------------------------
NOV1c          ----------------------------------------
NOV1d          ----------------------------------------
gi|13569928|   GNWDLCSTSCGGGFQKRIVQCVPSEGNKTEDQDQCLCDHK
gi|11493589|   DGPEECKDVN------------------------------
gi|10645199|   TGLEVCFS--------------------E----------
gi|15309931|   DGPEECKDVN------------------------------
gi|7656869|    ----------------------------------------

                       1690      1700      1710      1720
               ....|....|....|....|....|....|....|....|
NOV1a          ----------------------------------------
NOV1b          ----------------------------------------
NOV1c          ----------------------------------------
NOV1d          ----------------------------------------
```

```
gi|13569928|  PRPPEFKKCNQQACKKSADLLCTKDKLSASFCQTLKAMKK
gi|11493589|  ----------------------------KVAYCPLVLKFQF
gi|10645199|  ---P-------QF---------------S-ICEMRLAIAL
gi|15309931|  ----------------------------KVAYCPLVLKFQF
gi|7656869|   -------------------------------------

                        1730      1740      1750
                ....|....|....|....|....|....|....|..
NOV1a           ------------------------------------ (SEQ ID NO:2 )
NOV1b           ------------------------------------ (SEQ ID NO:4 )
NOV1c           ------------------------------------ (SEQ ID NO:6 )
NOV1d           ------------------------------------ (SEQ ID NO:8 )
gi|13569928|  CSVPTVRAECCFSCPQTHITHTQRQRRQRLLQKSKEL (SEQ ID NO:30 )
gi|11493589|  CSRAYFRQMCCKTCQGH------------------- (SEQ ID NO:31 )
gi|10645199|  CPRPAGRVHG---------------------------- (SEQ ID NO:32 )
gi|15309931|  CSRAYFRQMCCKTCHGH------------------- (SEQ ID NO:33 )
gi|7656869|   ------------------------------------ (SEQ ID NO:34 )
```

At page 32, please replace paragraph at lines 31-42 with the following new paragraph:

The presence of identifiable domains in NOV1, as well as all other NOVX proteins, was determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using ~~the~~ European Bioinformatics Institute Interpro. ~~website (http:www.ebi.ac.uk/interpro)~~. DOMAIN results for NOV1 as disclosed in Tables 1L-IO, were collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections. For Table 1E and all successive DOMAIN sequence alignments, fully conserved single residues are indicated by black shading or by the sign (|) and "strong" semi-conserved residues are indicated by grey shading or by the sign (+). The "strong" group of conserved amino acid residues may be any one of the following groups of amino acids: STA, NEQK (SEQ ID NO: 161), NHQK (SEQ ID NO: 162), NDEQ (SEQ ID NO: 163), QHRK (SEQ ID NO: 164), MILV (SEQ ID NO: 165),MILF (SEQ ID NO: 166), HY, FYW.

At page 33, please replace Table 1L with the following:

Table 1L. Domain Analysis of NOV1

~~gnl|Pfam|pfam01421,~~ Reprolysin, Reprolysin (M12B) family zinc metalloprotease. The members of this family are enzymes that cleave peptides. These proteases require zinc for catalysis. Members of this family are also known as adamalysins. Most members of this family are snake venom endopeptidases, but there are also some mammalian proteins, and fertilin. Fertilin and closely related proteins appear to not have some active site residues and may not be active enzymes. (SEQ ID NO:76)
CD-Length = 199 residues, 95.0% aligned
Score = 122 bits (307), Expect = 7e-29

```
Query:  378  DKKMMQNHG--HENITTYVLTILNMVSALFKDGTIGGNINIAIVGLILLEDEQPGLVISH  435
             |  |   +|     |   |  |+|+|+ +++      || + +||| +  |    + +
Sbjct:  10   DHGMFTKYGSDLNKIRQRVHQIVNLVNEIYRPL----NIRVVLVGLEIWSDGDK-ITVQG  64

Query:  436  HADHTLSSFCQWQSGLMGKDGTRHDHAILLTGLDICSWKNEPCDTLGFAPISGMCSKYRS  495
              |+ ||  | +|+   + |    ||+| ||||+|         +|+| | + ||||  ||
Sbjct:  65   DANDTLHRFLEWRETDLLKR-KSHDNAQLLTGIDF------DGNTIGAAYVGGMCSPKRS  117

Query:  496  CTINED---TGLGLAFTIAHESGHNFGMIHDGEGN-MCKKSEGNIMSPTLAGRNGVFSWS  551
               + +|     | +| |+||| ||| || ||      |+   | ||+|  +   |  +|
Sbjct:  118  VGVVQDHSPIVLLVAVTMAHELGHNLGMTHDDINKCTCEGGGGCIMNPVASSSPGKK-FS  176

Query:  552  PCSRQYLHKFLSTAQAICLADQ  573  (aa 378-573 of SEQ ID NO:2)
             ||     +||+  +  || ++
Sbjct:  177  NCSMDDYQQFLTKGKPQCLLNK  198  (SEQ ID NO:76)
```

At page 33, please replace Table 1M with the following:

Table 1M. Domain Analysis of NOV1

~~gnl|Smart|smart00209,~~ TSP1, Thrombospondin type 1 repeats; Type 1 repeats in thrombospondin-1 bind and activate TGF-beta. (SEQ ID NO:77)
CD-Length = 51 residues, 100.0% aligned
Score = 63.5 bits (153), Expect = 5e-11

```
Query:  668  WSDWSSWSPCSRTCGGGVSHRSRLCTNPNPSHGGKFCEGSTRTLKLCNSQKCP  720(of SEQ ID
NO:2)
             | +|| ||||| ||||||  |+| |  |    ||  | |     + || | ||
Sbjct:  1    WGEWSEWSPCSVTCGGGVQTRTRCCNPPPN--GGGPCTGPDTETRACNEQPCP  51 (SEQ ID NO:77)
```

At page 33, please replace Table 1N with the following:

Table 1N. Domain Analysis of NOV1

~~gnl|Pfam|pfam00090,~~ tsp_1, Thrombospondin type 1 domain. (SEQ ID NO:78)
CD-Length = 48 residues, 100.0% aligned
Score = 54.7 bits (130), Expect = 2e-08

```
Query:  669  SDWSSWSPCSRTCGGGVSHRSRLCTNPNPSHGGKFCEGSTRTLKLCNSQKC  719 (of SEQ ID NO:2)
             | || ||||| ||| |+  | | | +|    |||| | |  +  + |    |
Sbjct:  1    SPWSEWSPCSVTCGKGIRTRQRTCNSP---AGGKPCTGDAQETEACMMDPC  48  (SEQ ID NO:78)
```

At page 34, please replace Table 1O with the following:

Table 1O. Domain Analysis of NOV1

~~gnl|Pfam|pfam01562,~~ Pep_M12B_propep, Reprolysin family propeptide. This region is the propeptide for members of peptidase family M12B. The propeptide contains a sequence motif similar to the "cysteine switch" of the matrixins. This motif is found at the C terminus of the alignment but is not well aligned. repeats. (SEQ ID NO:79)
CD-Length = 117 residues, only 39.3% aligned
Score = 38.5 bits (88), Expect = 0.002

```
Query:  180  LRTSSSLVAPGFIVQTLGKTGTKSVQTLPPEDFCFYQGSLRSHRNS  225 (of SEQ ID NO:2)
             |  + ||+|| | | |    || .  +    +| |+|||  +  + ||
Sbjct:  2    LEKNRSLLAPDFTVTTYDDDGTLVTEHPLIQDHCYYQGYVEGYPNS  47  (SEQ ID NO:79)
```

At page 41 please replace Table 2C with the following:

Table 2C. BLAST results for NOV2

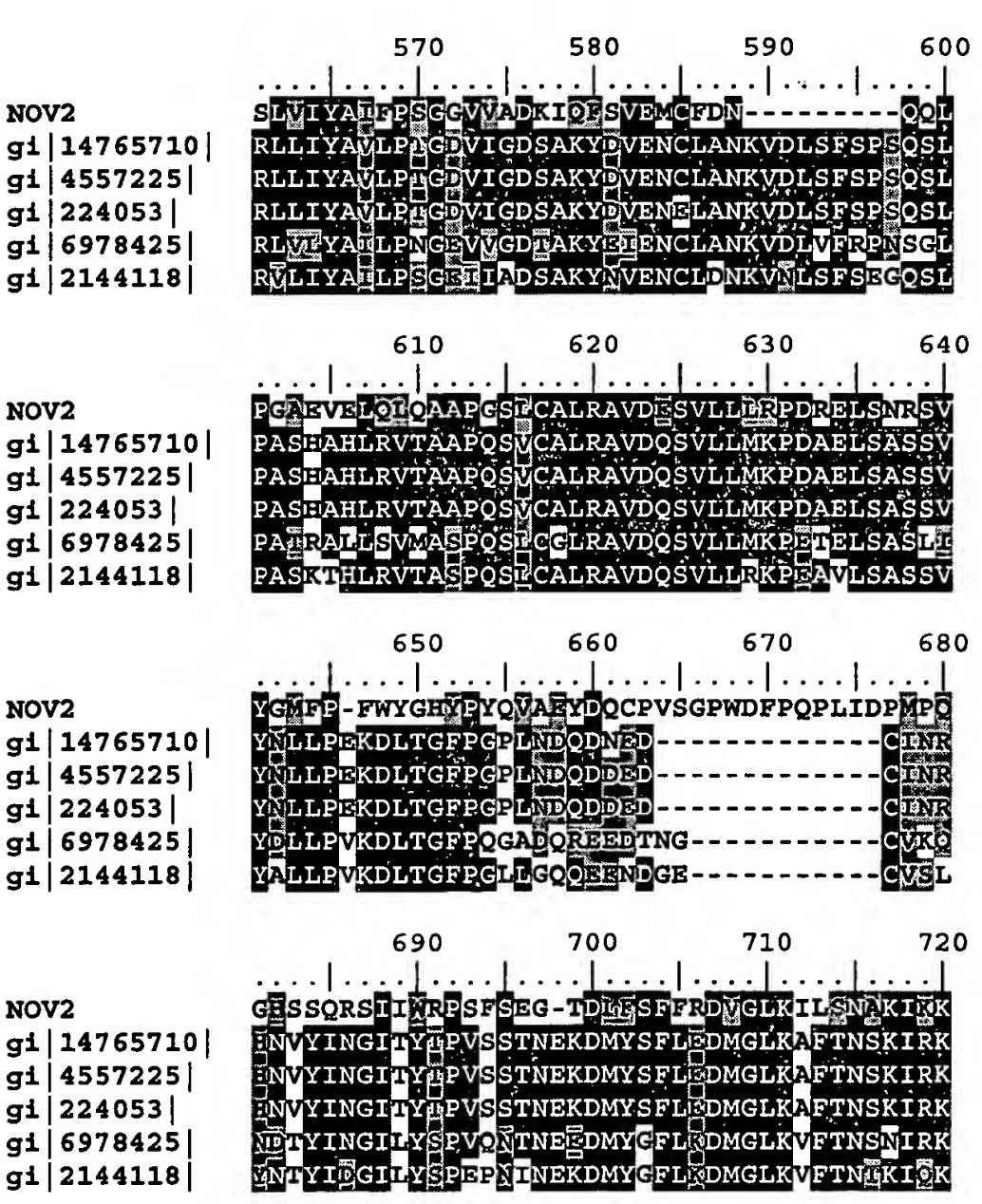
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
~~gi|14765710|ref|XP-006925.4|~~ XP 006925	alpha 2 macroglobulin precursor [Homo sapiens]	1474	593/1486 (39%)	870/1486 (57%)	0.0
~~gi|4557225|ref|NP 000005.1|~~ NP 000005	alpha 2 macroglobulin precursor [Homo sapiens]	1474	591/1486 (39%)	869/1486 (57%)	0.0
~~gi|224053|prf||1009174A~~ 1009174A	macroglobulin alpha2 [Homo sapiens]	1450	585/1471 (39%)	861/1471 (57%)	0.0

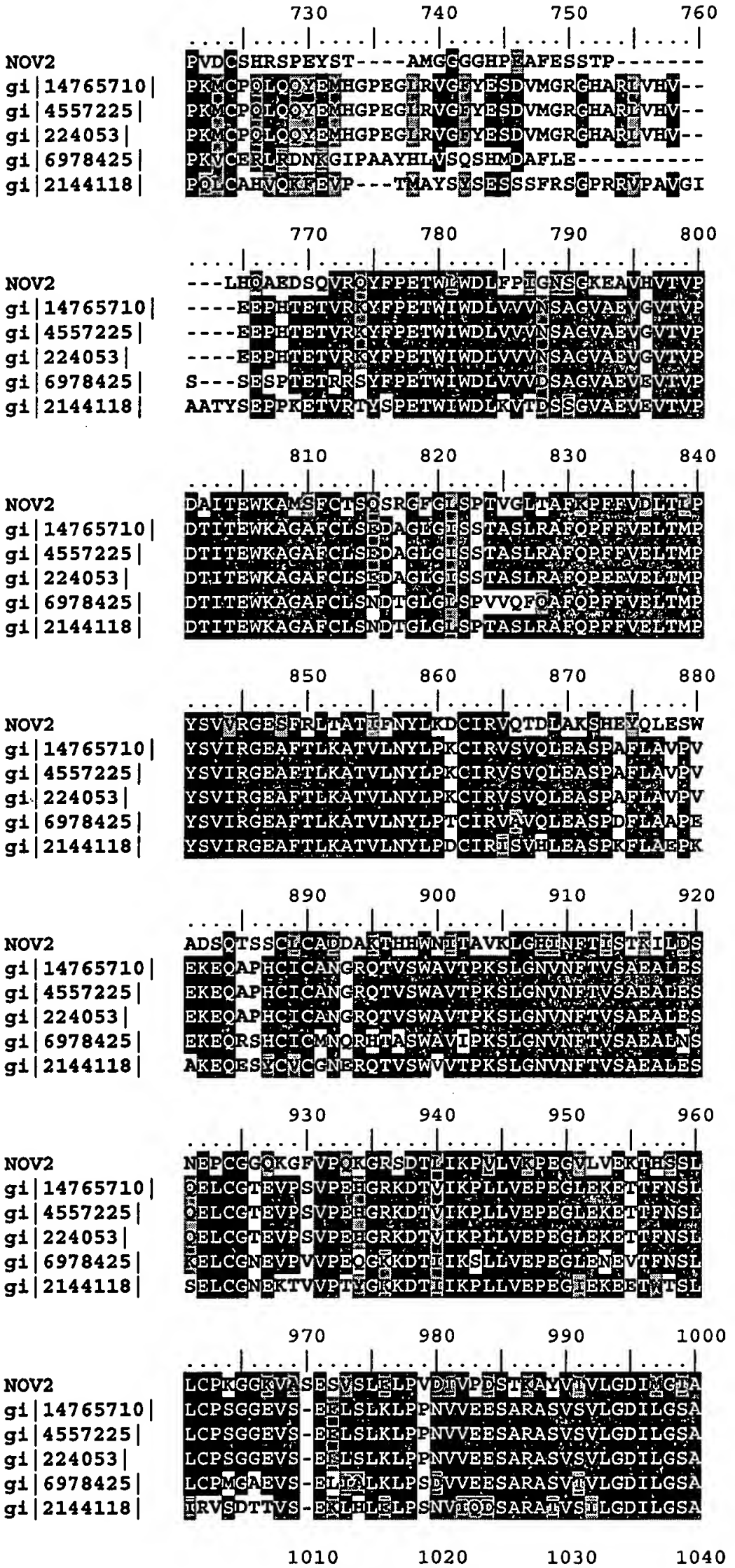
~~gi|6978425|ref|NP_036620.1|~~ NP_036620	alpha-2-macroglobulin [Rattus norvegicus]	1472	578/1483 (38%)	867/1483 (57%)	0.0
~~gi|2144118|pir||JC5143~~ JC5143	alpha-macroglobulin precursor - guinea pig	1476	570/1495 (38%)	858/1495 (57%)	0.0

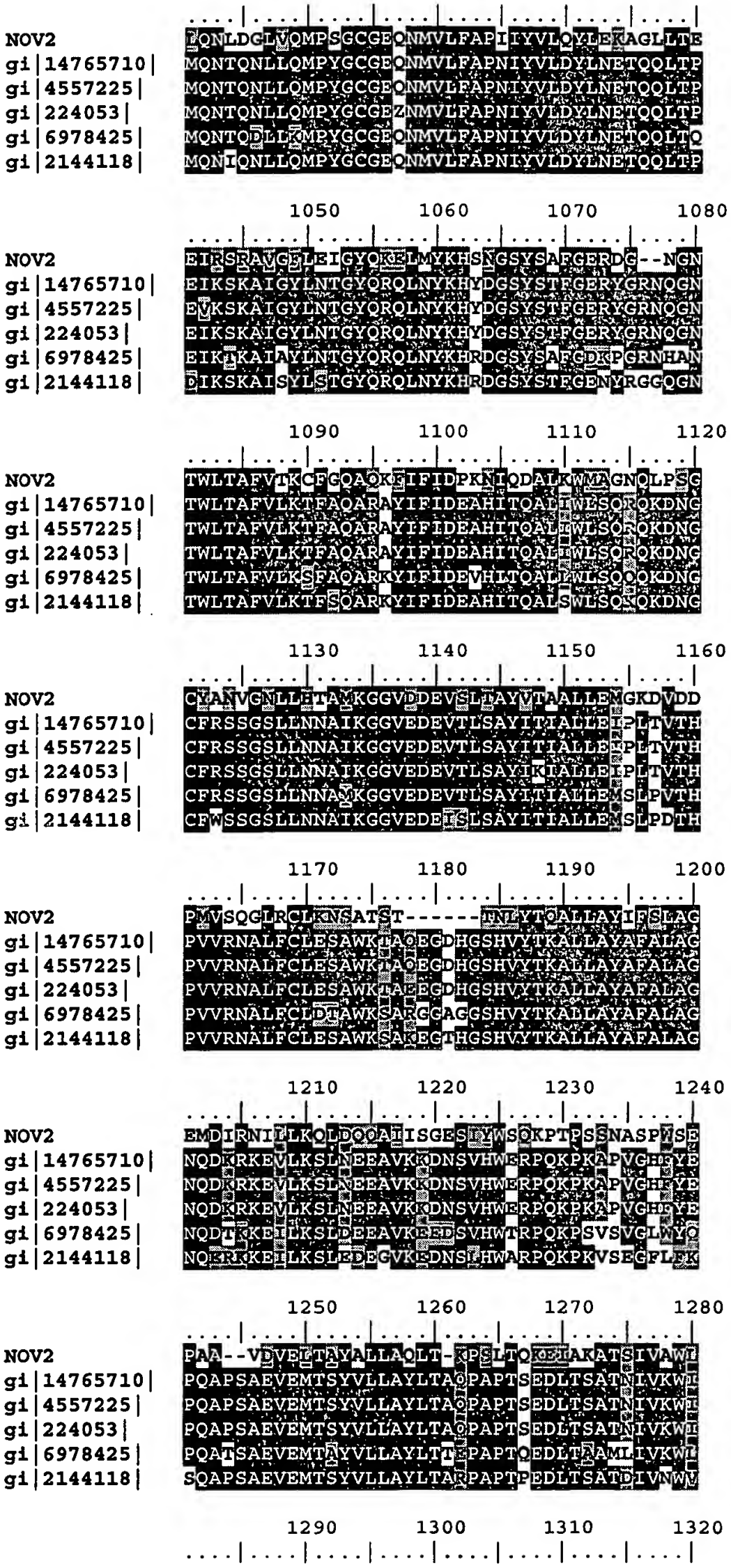
At page 41 please replace Table 2D with the following:

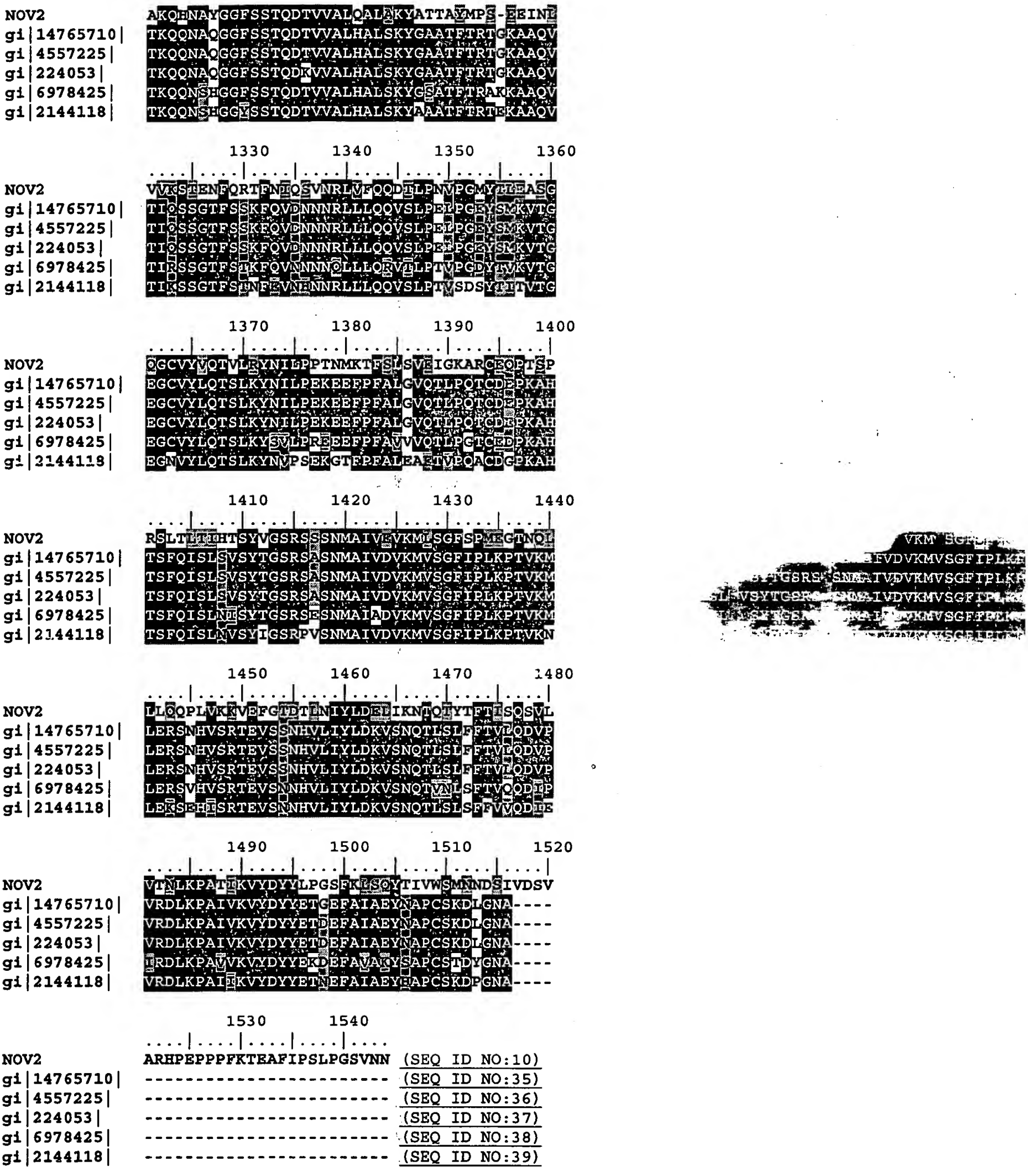
Table 2D. ClustalW Analysis of NOV2

1) NOV2 (SEQ ID NO:10)
2) ~~gi\|14765710\|ref\|XP_006925.4\|~~ **gi\|14765710\|** XP_006925 alpha 2 macroglobulin precursor [Homo sapiens] (SEQ ID NO:35)
2) ~~gi\|4557225\|ref\|NP_000005.1\|~~ **gi\|4557225\|** NP_000005 alpha 2 macroglobulin precursor [Homo sapiens] (SEQ ID NO:36)
3) ~~gi\|224053\|prf\|\|1009174A~~ **gi\|224053\|** 1009174A macroglobulin alpha2 [Homo sapiens] (SEQ ID NO:37)
4) ~~gi\|6978425\|ref\|NP_036620.1\|~~ **gi\|6978425\|** NP_036620 alpha-2-macroglobulin [Rattus norvegicus] (SEQ ID NO:38)
5) ~~gi\|2144118\|pir\|\|JC5143~~ **gi\|2144118\|** JC5143 alpha-macroglobulin precursor - guinea pig (SEQ ID NO:39)




730 740 750 760
NOV2 PVDCSHRSPEYST----AMGGGGHPEAFESSTP-------
gi|14765710| PKMCPQLQQYEMHGPEGLRVGFYESDVMGRGHARLVHV--
gi|4557225| PKMCPQLQQYEMHGPEGLRVGFYESDVMGRGHARLVHV--
gi|224053| PKMCPQLQQYEMHGPEGLRVGFYESDVMGRGHARLVHV--
gi|6978425| PKVCERLRDNKGIPAAYHLVSQSHMDAFLE----------
gi|2144118| PQLCAHVQKFEVP---TMAYSYSESSSFRSGPRRVPAVGI
770 780 790 800
NOV2 ---LHQAEDSQVRQYFPETWLWDLFPIGNSGKEAVHVTVP
gi|14765710| ----EEPHTETVRKYFPETWIWDLVVVNSAGVAEVGVTVP
gi|4557225| ----EEPHTETVRKYFPETWIWDLVVVNSAGVAEVGVTVP
gi|224053| ----EEPHTETVRKYFPETWIWDLVVVNSAGVAEVGVTVP
gi|6978425| S---SESPTETRRSYFPETWIWDLVVVDSAGVAEVEVTVP
gi|2144118| AATYSEPPKETVRTYSPETWIWDLKVTDSSGVAEVEVTVP
810 820 830 840
NOV2 DAITEWKAMSFCTSQSRGFGLSPTVGLTAFKPFFVDLTLP
gi|14765710| DTITEWKAGAFCLSEDAGLGISSTASLRAFQPFFVELTMP
gi|4557225| DTITEWKAGAFCLSEDAGLGISSTASLRAFQPFFVELTMP
gi|224053| DTITEWKAGAFCLSEDAGLGISSTASLRAFQPEEVELTMP
gi|6978425| DTITEWKAGAFCLSNDTGLGLSPVVQFQAFQPFFVELTMP
gi|2144118| DTITEWKAGAFCLSNDTGLGLSPTASLRAFQPFFVELTMP
850 860 870 880
NOV2 YSVVRGESFRLTATIFNYLKDCIRVQTDLAKSHEYQLESW
gi|14765710| YSVIRGEAFTLKATVLNYLPKCIRVSVQLEASPAFLAVPV
gi|4557225| YSVIRGEAFTLKATVLNYLPKCIRVSVQLEASPAFLAVPV
gi|224053| YSVIRGEAFTLKATVLNYLPKCIRVSVQLEASPAFLAVPV
gi|6978425| YSVIRGEAFTLKATVLNYLPTCIRVAVQLEASPDFLAAPE
gi|2144118| YSVIRGEAFTLKATVLNYLPDCIRISVHLEASPKFLAEPK
890 900 910 920
NOV2 ADSQTSSCLCAQDAKTHHWNITAVKLGHINFTISTKILDS
gi|14765710| EKEQAPHCICANGRQTVSWAVTPKSLGNVNFTVSAEALES
gi|4557225| EKEQAPHCICANGRQTVSWAVTPKSLGNVNFTVSAEALES
gi|224053| EKEQAPHCICANGRQTVSWAVTPKSLGNVNFTVSAEALES
gi|6978425| EKEQRSHCICMNQRHTASWAVIPKSLGNVNFTVSAEALNS
gi|2144118| AKEQESYCVCGNERQTVSWVVTPKSLGNVNFTVSAEALES
930 940 950 960
NOV2 NEPCGGQKGFVPQKGRSDTLIKPVLVKPEGVLVEKTHSSL
gi|14765710| QELCGTEVPSVPEHGRKDTVIKPLLVEPEGLEKETTFNSL
gi|4557225| QELCGTEVPSVPEHGRKDTVIKPLLVEPEGLEKETTFNSL
gi|224053| QELCGTEVPSVPEHGRKDTVIKPLLVEPEGLEKETTFNSL
gi|6978425| KELCGNEVPVVPEQGKKDTIIKSLLVEPEGLENEVTFNSL
gi|2144118| SELCGNEKTVVPTYGKKDTIIKPLLVEPEGIEKEETWTSL
970 980 990 1000
NOV2 LCPKGGKVASESVSLELPVDIVPDSTKAYVIVLGDIMGTA
gi|14765710| LCPSGGEVS-EELSLKLPPNVVEESARASVSVLGDILGSA
gi|4557225| LCPSGGEVS-EELSLKLPPNVVEESARASVSVLGDILGSA
gi|224053| LCPSGGEVS-EELSLKLPPNVVEESARASVSVLGDILGSA
gi|6978425| LCPMGAEVS-ELLALKLPSDVVEESARASVIVLGDILGSA
gi|2144118| IRVSDTTVS-EKLHLELPSNVIQDSARAIVSILGDILGSA
1010 1020 1030 1040


NOV2
gi|14765710|
gi|4557225|
gi|224053|
gi|6978425|
gi|2144118|
1050
1060
1070
1080
1090
1100
1110
1120
1130
1140
1150
1160
1170
1180
1190
1200
1210
1220
1230
1240
1250
1260
1270
1280
1290
1300
1310
1320


NOV2
gi|14765710|
gi|4557225|
gi|224053|
gi|6978425|
gi|2144118|
1330 1340 1350 1360
1370 1380 1390 1400
1410 1420 1430 1440
1450 1460 1470 1480
1490 1500 1510 1520
1530 1540
ARHPEPPPPFKTEAFIPSLPGSVNN (SEQ ID NO:10)
---------- (SEQ ID NO:35)
---------- (SEQ ID NO:36)
---------- (SEQ ID NO:37)
---------- (SEQ ID NO:38)
---------- (SEQ ID NO:39)

Pages 45, please replace Table 2E with the following

Table 2E Domain Analysis of NOV2

~~gnl|Pfam|pfam00207,~~ A2M, Alpha-2-macroglobulin family. This family includes the C-terminal region of the alpha-2-macroglobulin family.
(SEQ ID NO:80)
CD-Length = 751 residues, 98.5% aligned
Score = 563 bits (1451), Expect = 2e-161

```
Query:  728   EDSQVRQYFPETWLWDLFPIGNSGKEAVHVTVPDAITEWKAMSFCTSQSRGFGLSPTVGL  787
              +|  +| ||||+|||++  +  |    |++|+||+|| |+ ++   | ++|  ++  | |
Sbjct:  4     DDITIRSYFPESWLWEVEEVDRSPVLTVNITLPDSITTWEILAVSLSNTKGLCVADPVEL  63

Query:  788   TAFKPFFVDLTLPYSVVRGESFRLTATIFNYL-KDCIRVQTDLAKSHEYQLESWADSQTS  846
              | |+ ||++| |||||||||   | | ++|||    |+|          |||     |
Sbjct:  64    TVFQDFFLELRLPYSVVRGEQVELRAVLYNYLPSQDIKV--------VVQLEVEPLCQAG  115

Query:  847   SCLCADDAKTHHWNITAVKLGHINFTISTKILDSNEPCGGQKGFVPQKGRSDTLIKPVLV  906
               |  |         ++    |  ++| +    | |          ||+    | ++| + |
Sbjct:  116   FCSLATQRTRSSQSVRPKSLSSVSFPVVVVPLASGLSLVEVVASVPEFFVKDAVVKTLKV  175

Query:  907   KPEGVLVEKTHSSLLCP---KGGKVASESVSLELPVDIVPD-STKAYVTVLGDIMGTALQ  962
              +|||   |+| |||| |    || +    |       | |||   +| ++| || +  |+|
Sbjct:  176   EPEGARKEETVSSLLLPPEHLGGGLEVSEVPALKLPDDVPDTEAEAVISVQGDPVAQAIQ  235

Query:  963   N------LDGLVQMPSGCGEQNMVLFAPIIYVLQYLEKAGLLTE---EIRSRAVGFLEIG  1013
              |      |+ |+++|||||||||+  || +||| ||++     +   + + +|+  +  |
Sbjct:  236   NTLSGEGLNNLLRLPSGCGEQNMIYMAPTVYVLHYLDETWQWEKPGTKKKQKAIDLINKG  295

Query:  1014  YQKELMYKHSNGSYSAFGERDGNGNTWLTAFVTKCFGQAQKFIFIDPKNIQDALKW-MAG  1072
              ||++| |+ ++|||+||  |    +|||||| | | ||+ ++|||  ++|  |+|| +
Sbjct:  296   YQRQLNYRKADGSYAAFLHRA--SSTWLTAFVLKVFSQARNYVFIDEEHICGAVKWLILN  353

Query:  1073  NQLPSGCYANVGNLLHTAMKGGVDD----EVSLTAYVTAALLEMGKDVDDPMVSQGLRCL  1128
               |    | +    | ++| |||||  |    ||+|||++| ||||        |+|+  |  |
Sbjct:  354   QQKDDGVFRESGPVIHNEMKGGVGDDAEVEVTLTAFITIALLEAKLVCISPVVANALSIL  413

Query:  1129  KNSATSTTN------LYTQALLAYIFSLAGEMDIRNILLKQLDQQAIISGESIYWS--QK  1180
              | |      |       +|| || ||  +||| +      +|| | ++   +    +|   ||
Sbjct:  414   KASDYLLENYANGQRVYTLALTAYALALAGVLHKLKEILKSLKEELYKALVKGHWERPQK  473

Query:  1181  PTPSSNASPWSEPAAVDVELTAYALLAQLTKPSLTQKEIAKATSIVAWLAKQHNAYGGFS  1240
              |  +        +| |  ||+|+|||||| ||    |   ++  |  +| || +|     |||
Sbjct:  474   PKDAPGHPYSPQPQAAAVEMTSYALLALLT--LLPFPKVEMAPKVVKWLTEQQYYGGGFG  531

Query:  1241  STQDTVVALQALAKYATTAYMPSE-EINLVVKSTEN-FQRTFNIQSVNRLVFQQDTLP-N  1297
              ||||||+|||||+||          |  +++ ++|     |+  | | + |  + +   || |
Sbjct:  532   STQDTVMALQALSKYGIATPTHKEKNLSVTIQSPSGSFKSHFQILNNNAFLLRPVELPLN  591

Query:  1298  VPGMYTLEASGQGCVYVQTVLRYNILPPTNMKTFSLSVEIGKARCEQPTSPR-SLTLTIH  1356
                  | + +|||  + + |  || +|    |    | | +|      | +|   + |  |+|
Sbjct:  592   EGFTVTAKVTGQGTLTLVTTYRYKVLDKKNTFCFDLKIETVPDTCVEPKGAKNSDYLSIC  651

Query:  1357  TSYVGSRSSSNMAIVEVKMLSGFSPMEGT--N*QLLLQQ*PLVKKVEFGTDTLNIYLDELIK  1414
              | | |||| | |||  ++ ||+|| |++                | | |   + + +|||++
Sbjct:  652   TRYAGSRSDSGMAIADISMLTGFIPLKPDLKKLENGVDRYVSKYEIDGNHVLLYLDKVSH  711

Query:  1415  -NTQTYTFTISQSVLVTNLKPATIKVYDYYLP  1445  (of SEQ ID NO:10)
               |+   | | |   |  |+||++|||||| |
```

```
Sbjct:  712   SETECVGFKIHQDFEVGLLQPASVKVYDYYEP  743  (SEQ ID NO:80)
```

Pages 46, please replace Table 2F with the following:

Table 2F Domain Analysis of NOV2

~~gnl|Pfam|pfam01835,~~ A2M_N, Alpha-2-macroglobulin family N-terminal region. This family includes the N-terminal region of the alpha-2-macroglobulin family. (SEQ ID NO:81)
CD-Length = 620 residues, 98.4% aligned
Score = 236 bits (603), Expect = 5e-63

```
Query:  5     LLLGMLALSPAIAEEL--PNYLVTLPARLNFPSVQKVCLDLSPGYSDVKFTVTLETKDKT  62
              ||  +| |       | | |+| +|+ |   + +|||+ |       |  ||+| +
Sbjct:  2     LLWLLLLLLLFFDSSLQKPRYMVIVPSILRTETPEKVCVQLHDLNETVTVTVSLHSFPGK  61

Query:  63    QKLLEYSGLK---KRHLHCISFLVPPPA---GGTEEVATIRVSGVGNNISFEEKKKVLIQ  116
              + |     +    |   ||+|| || |         | + + |    |   +|+||  ||+
Sbjct:  62    RNLSSLFTVLLSSKDLFHCVSFTVPQPGLFKSSKGEESFVVVQVKGPTHTFKEKVTVLVS  121

Query:  117   RQGNGTFVQTDKPLYTPGQQVYFRIVTMDSNFVPVNDKYSMVELQDPNSNRIAQWLEVVP  176
               +    |+|||||+||||| | +|+ ++| |  |+|+   +| ++||  ||+ ||
Sbjct:  122   SRRGLVFIQTDKPIYTPGQTVRYRVFSVDENLRPLNELI-LVYIEDPEGNRVDQWEVNKL  180

Query:  177   EQGIVDLSFQLAPEAMLGTYTVAV---AEGKTFGT--FSVEEYVLSPFLLLLSSVLPKFK  231
              | ||  ||| +  | + ||+ +   +  ++  |  | |+||              +
Sbjct:  181   EGGIFQLSFPIPSEPIQGTWKIVARYESGPESNYTHYFEVKEY---------VLPSFEVS  231

Query:  232   VEVVEPKELSTVQESFLVKICCRYTYGKPMLGAVQVSVCQKANTYWYREVEREQLPDKCR  291
              +  +|       + | | || |||||||+ |   |     |       |  +++|
Sbjct:  232   ITPPKPFIYYDNFKEFEVTICARYTYGKPVPGVAYVRFGVK------DEDGKKELLAGLE  285

Query:  292   NLSGQTDKTG--CFSAPVDMATFDLIGYAY-SHQINIVATVVEEGTGVEANA-TQNIYIS  347
                +   |  |  | |  | +    |          + +   |+|   |    |    | |
Sbjct:  286   ERAKLLDGNGEICLSQEVLLKELQLKNEDLEGKSLYVAVAVIESEGGDMEEAELGGIKIV  345

Query:  348   PQMGSMTFEDTSNFYHPNFPFSGKMLLKFPQGGVLPCKNHLVFLVIYGTNGTFNQTLVTD  407
                 + |  | + + |  ||  |+|+  | |   |  |  |   +   + ++     ||
Sbjct:  346   RSPYKLKFVKTPSHFKPGIPFFLKVLVVDPDGS--PAPNVPVK--VSAQDASYYSNGTTD  401

Query:  408   NNGLAPFTLETSGWNGTDVSLEGKFQMEDLVYNPEQVPRYYQNAYLHLRPFYSTTRSFLG  467
               +||| |++ ||    + +|+  +   ++|    +         ||  +    | +   |
Sbjct:  402   EDGLAQFSINTS--GISSLSITVRTNHKELPEEVQAHAEAQATAYSTVSL--SKSYIHLS  457

Query:  468   IHRLNGPLKCGQPQEVLVDYYIDPADASPDQEISFSYYLIGKGSLVMEGQKHLNSKKKGL  527
              | |    | ||       ++ +        + + | | ++ || +|  |++     ++
Sbjct:  458   IER---TLPCGPGVGEQANFILRGKSLGELKILHFYYLIMSKGKIVKTGRE----PREPG  510

Query:  528   KASFSLSLTFTSRLAPDPSLVIYAIFPSGGVVADKIQFSVEMCFDN----------QQL  576
              +  ||||+  |  |||   || | | | | |||| +   || |  |           +|
Sbjct:  511   QGLFSLSIPVTPDLAPSFRLVAYYILPQGEVVADSVWIDVEDCCANKLDLSFSPSKDYRL  570

Query:  577   PGAEVELQLQAAPGSLCALRAVDESVLLLRPDRELSNRSVY  617  (of SEQ ID NO:10)
              |  +|+|+++| | || ||||||++| ||+|  +||   ||
Sbjct:  571   PAQQVKLRVEADPQSLVALRAVDQAVYLLKPKAKLSMSKVY  611  (SEQ ID NO:81)
```

At page 52 please replace Table 3E with the following:

Table 3E. BLAST results for NOV3

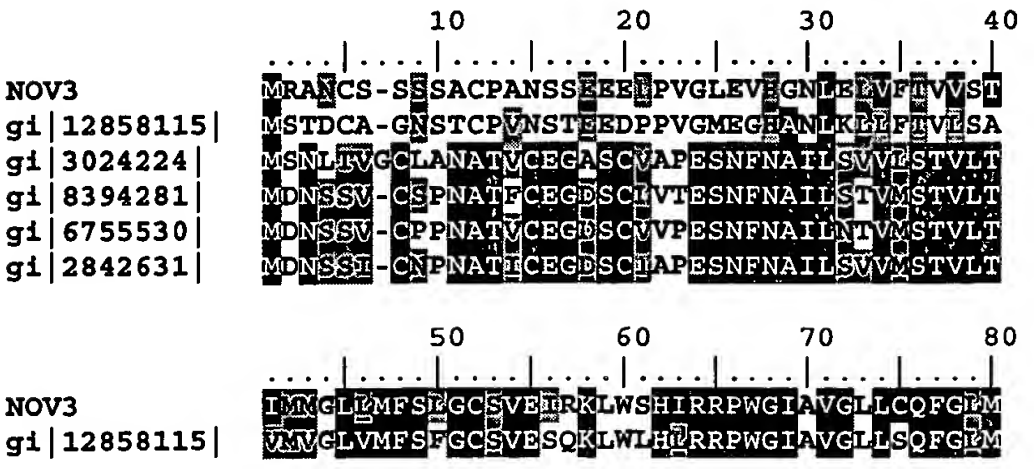
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
~~gi|12858115|dbj|BAB31203.1| (AK018423)~~ BAB31203	putative [Mus musculus]	373	187/310 (60%)	226/310 (72%)	6e-87
~~gi|3024224|sp|Q28727|NTCI_RABIT~~ NP_058918	ILEAL SODIUM/BILE ACID COTRANSPORTER (ILEAL NA(+)/BILE ACID COTRANSPORTER) (NA+ DEPENDENT ILEAL BILE ACID TRANSPORTER) (ILEAL SODIUM-DEPENDENT BILE ACID TRANSPORTER) (ISBT) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE, ILEAL)	347	116/279 (41%)	173/279 (61%)	1e-52
~~gi|8394281|ref|NP_058918.1|~~ NP_035518	solute carrier family 10, member 2 [Rattus norvegicus]	348	130/344 (37%)	195/344 (55%)	2e-52
~~gi|6755530|ref|NP_035518.1|~~ NP_35518	solute carrier family 10, member 2 [Mus musculus]	348	125/313 (39%)	191/313 (60%)	4e-52
~~gi|6755530|ref|NP_035518.1|~~ NP_35518	solute carrier family 10, member 2 [Mus musculus]	348	125/313 (39%)	191/313 (60%)	4e-52

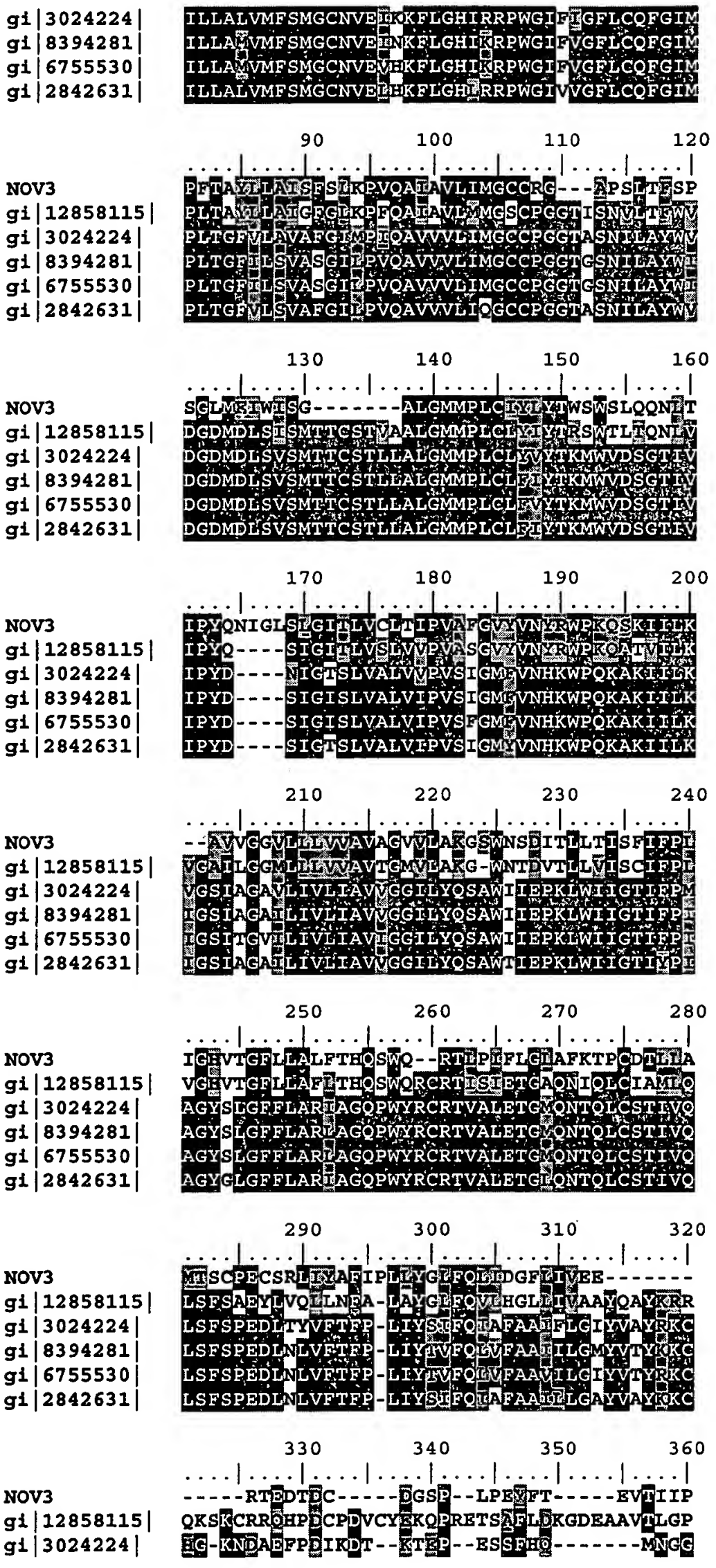
~~gi|2842631|sp|Q60414|NTCI_CRIGR~~ Q60414	ILEAL SODIUM/BILE ACID COTRANSPORTER (ILEAL NA(+)/BILE ACID COTRANSPORTER) (NA+ DEPENDENT ILEAL BILE ACID TRANSPORTER) (ILEAL SODIUM-DEPENDENT BILE ACID TRANSPORTER) (ISBT) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE, ILEAL)	348	121/306 (39%)	185/306 (59%)	4e-52

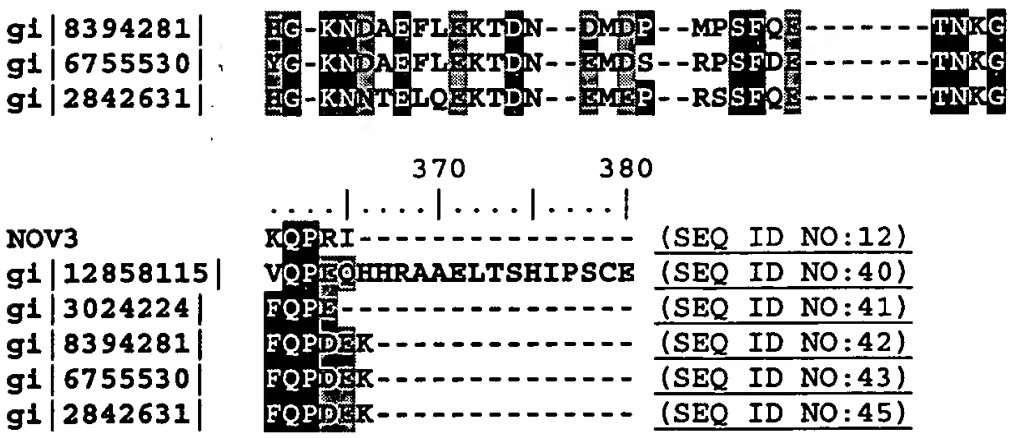
At page 53 please replace Table 3F with the following:

Table 3F. ClustalW Analysis of NOV3

1) NOV3 (SEQ ID NO:12)
3) ~~gi\|12858115\|dbj\|BAB31203.1\|~~ gi\|12858115\| BAB31203 (AK018423) putative [Mus musculus] (SEQ ID NO:40)
4) ~~gi\|3024224\|sp\|Q28727\|NTCI_RABIT~~ gi\|3024224\| NP058918 ILEAL SODIUM/BILE ACID COTRANSPORTER (ILEAL NA(+)/BILE ACID COTRANSPORTER) (NA+ DEPENDENT ILEAL BILE ACID TRANSPORTER) (ILEAL SODIUM-DEPENDENT BILE ACID TRANSPORTER) (ISBT) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE, ILEAL) (SEQ ID NO:41)
5) ~~gi\|8394281\|ref\|NP_058918.1\|~~ gi\|8394281\| NP035518 solute carrier family 10, member 2 [Rattus norvegicus] (SEQ ID NO:42)
6) ~~gi\|6755530\|ref\|NP_035518.1\|~~ gi\|6755530\| NP035518 solute carrier family 10, member 2 [Mus musculus] (SEQ ID NO:43)
7) ~~gi\|6755530\|ref\|NP_035518.1\|~~ gi\|6755530\| NP035518 solute carrier family 10, member 2 [Mus musculus] (SEQ ID NO:44)
8) ~~gi\|2842631\|sp\|Q60414\|NTCI_CRIGR~~ gi\|2842631\| Q60414 ILEAL SODIUM/BILE ACID COTRANSPORTER (ILEAL NA(+)/BILE ACID COTRANSPORTER) (NA+ DEPENDENT ILEAL BILE ACID TRANSPORTER) (ILEAL SODIUM-DEPENDENT BILE ACID TRANSPORTER) (ISBT) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE, ILEAL) (SEQ ID NO:45)




gi|3024224|
gi|8394281|
gi|6755530|
gi|2842631|
90 100 110 120
NOV3
gi|12858115|
gi|3024224|
gi|8394281|
gi|6755530|
gi|2842631|
130 140 150 160
NOV3
gi|12858115|
gi|3024224|
gi|8394281|
gi|6755530|
gi|2842631|
170 180 190 200
NOV3
gi|12858115|
gi|3024224|
gi|8394281|
gi|6755530|
gi|2842631|
210 220 230 240
NOV3
gi|12858115|
gi|3024224|
gi|8394281|
gi|6755530|
gi|2842631|
250 260 270 280
NOV3
gi|12858115|
gi|3024224|
gi|8394281|
gi|6755530|
gi|2842631|
290 300 310 320
NOV3
gi|12858115|
gi|3024224|
gi|8394281|
gi|6755530|
gi|2842631|
330 340 350 360
NOV3
gi|12858115|
gi|3024224|



Page 55, please replace Table 3G with the following

Table 3G Domain Analysis of NOV3

~~gnl|Pfam|pfam01758,~~ SBF, Sodium Bile acid symporter family. This family consists of Na+/bile acid co-transporters. These transmembrane proteins function in the liver in the uptake of bile acids from portal blood plasma a process mediated by the co-transport of Na+. Also in the family is ARC3 from S. cerevisiae this is a putative transmembrane protein involved in resistance to arsenic compounds. (SEQ ID NO:82)
CD-Length = 186 residues, 80.1% aligned
Score = 75.9 bits (185), Expect = 3e-15

```
Query:  39   TIMMGLLMFSLGCSVEIRKLWSHIRRPWGIAVGLLCQFGLMPFTAYLLAIS-FSLKPVQA  97
Sbjct:  1    ALGLFLMMFSMGLKVRFEDLKEALRRPKALILGLLLQWIIMPLLMFILAWLLLRLPPELA  60

Query:  98   IAVLIMGCCRG---APSLTFSPSGLMEIWIS-------GALGMMPLCIYLYTWSWSLQQN  147
Sbjct:  61   TGLILVGCAPGGAMSNVWTYLAKGDVELSVVMVALSTLLAPLVTPLLSFLLAGLL-----  115

Query:  148  LTIPYQNIGLSLGITLVCLTIPVAFGVYVNYRWP  181  (of SEQ ID NO:12)
Sbjct:  116  VHVDAVSPWSLIKSVLVYVIIPLIAGMLTRYFLP  149  (SEQ ID NO 82)
```

At page 61, please replace Table 4C with the following:

Table 4C. BLAST results for NOV4

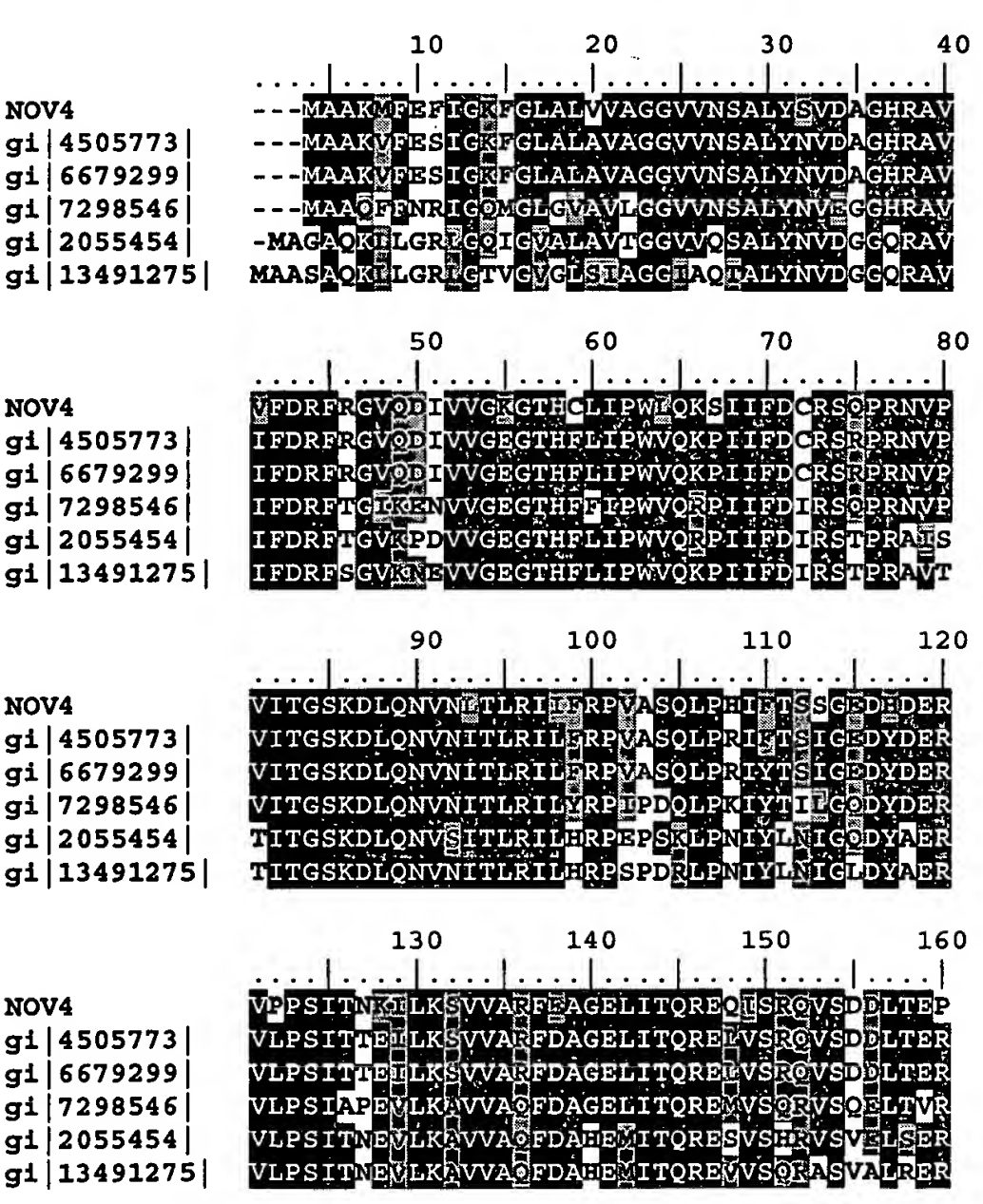
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
~~gi|4505773|ref|NP_0~~ ~~02625.1|~~ NP_002625	prohibitin [Homo sapiens]	272	236/270 (87%)	251/270 (92%)	e-123
~~gi|92643|pir||A3968~~ ~~2~~ A39682	prohibitin - rat	272	235/270 (87%)	251/270 (92%)	e-123

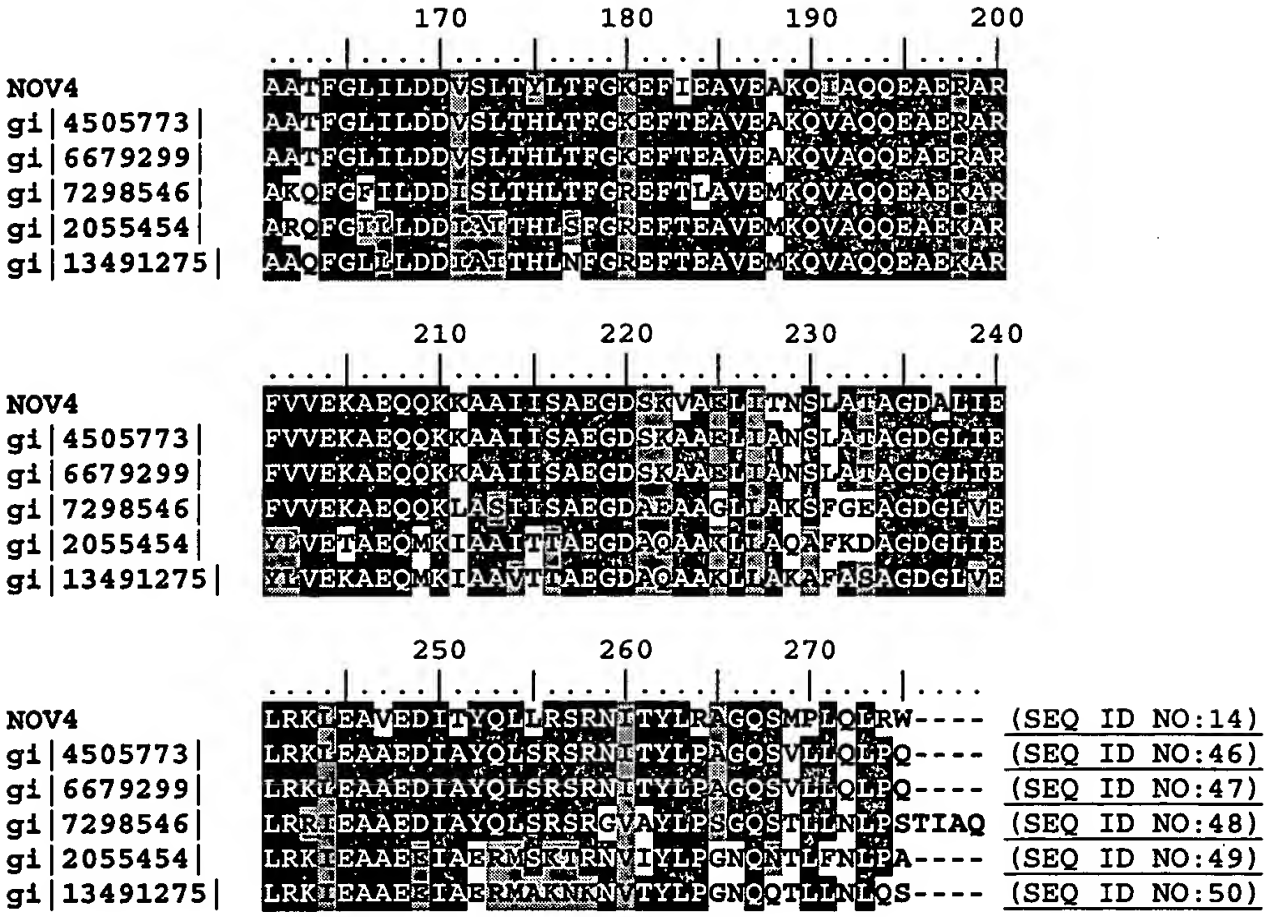
~~gi|7298546|gb|AAF53765.1| (AE003661)~~ AAF53765	l(2)37Cc gene product [Drosophila melanogaster]	276	178/270 (65%)	220/270 (80%)	8e-96
~~gi|2055454|gb|AAB53231.1| (U97204)~~ AAB53231	prohibitin-like molecule TC-PRO-1 [Toxocara canis]	274	153/264 (57%)	209/264 (78%)	9e-80
~~gi|13491275|gb|AAK27865.1| (AC087079)~~ AAK27865	Hypothetical protein Y37E3.9 [Caenorhabditis elegans]	275	154/270 (57%)	210/270 (77%)	6e-79

At page 61 please replace Table 4D with the following:

Table 4D ClustalW Analysis of NOV4

1) NOV4 (SEQ ID NO:14)
2) ~~gi|4505773|ref|NP_002625.1|~~ NP_002625 **gi|4505773|** prohibitin [Homo sapiens] (SEQ ID NO:46)
3) ~~gi|92643|pir||A39682~~ A39682 **gi|6679299|** prohibitin - rat (SEQ ID NO:47)
4) ~~gi|7298546|gb|AAF53765.1|~~ AAF53765 (AE003661) **gi|7298546|** l(2)37Cc gene product [Drosophila melanogaster] (SEQ ID NO:48)
5) ~~gi|2055454|gb|AAB53231.1|~~ AAB53231 (U97204) **gi|2055454|** prohibitin-like molecule TC-PRO-1 [Toxocara canis] (SEQ ID NO:49)
6) ~~gi|13491275|gb|AAK27865.1|~~ AAK27865 (AC087079) **gi|13491275|** Hypothetical protein Y37E3.9 [Caenorhabditis elegans] (SEQ ID NO:50)





At page 62 please replace Table 4E with the following:

Table 4E. Domain Analysis of NOV4

~~gnl|Pfam|pfam01145,~~ Band_7, SPFH domain / Band 7 family. This family also includes proteins with high blast scores to known Band 7 protein: HflC from E. coli HflK from E. coli, and Prohibitin family members (SEQ ID NO:83)
CD-Length = 191 residues, 91.6% aligned
Score = 157 bits (397), Expect = 7e-40

```
Query:  28   YSVDAGHRAVVFDRFRGVQDIVVGKGTHCLIPWLQKSIIFDCRSQPRNVPVITGSKDLQN  87
Sbjct:  17   KIVKEYERGVIFRLGRYVRQ-VVGPGLHFIIPFIDTVKKVDLRTVVYDVPSQEIITKDNV  75

Query:  88   VNLTLRIIFRPVASQLPHIFTSSGEDHDERVPPSITNKILKSVVARFEAGELITQREQIS  147
Sbjct:  76   VVIVDAVVYYRVVDPLKAVYEVED---AERALPQLAQTTLRNVIGQFTLDEILTERERIN  132

Query:  148  RQVSDDLTEPAATFGLILDDVSLTYLTFGKEFIEAVEAKQIAQQEAERARFVVEKAEQQK  207
Sbjct:  133  SQLREILDEATDPWGIKVERVEIKDIRLPEEVQRAMAAQMEAEREA-RAKILEAEGEQEA  191
```

Query: (aa 28-207 of SEQ ID NO:14)

Sbjct: (SEQ ID NO:83)

At page 63, please replace Table 4F with the following:

Table 4F. Domain Analysis of NOV4

~~gnl|Smart|smart00244,~~ PHB, prohibitin homologues; prohibitin homologues (SEQ ID NO:84)
CD-Length = 160 residues, 98.8% aligned
Score = 97.4 bits (241), Expect = 9e-22

```
Query:  28   YSVDAGHRAVVFDRFRGVQDIVVGKGTHCLIPWLQKSIIFDCRSQPRNVPVITG-SKDLQ  86
             + |        | +|    |   |+| | | +||++       | |+|   +||      +||
Sbjct:  3    FYVIGEGERGVVERLGRVLK-VLGPGLHFVIPFIDDVKRVDLRAQTDDVPPQEVITKDNV  61

Query:  87   NVNLTLRIIFRPVASQLPHIFTSSGEDHDERVPPSITNKILKSVVARFEAGELIT-QREQ  145
              |++   + +| |    |  ++     | | |    +    |+||+ +    ||+|.+||+
Sbjct:  62   TVSVDAVVYYR-VLDPLKAVYGV--LDADYRALRQLAQTTLRSVIGKRTLDELLTDEREK  118

Query:  146  ISRQVSDDLTEPAATFGLILDDVSLTYLTFGKEFIEAVEAKQ  187 (of SEQ ID NO:14)
             ||  + ++| | |  +|+ ++|| +  +   +|  ||+||+|
Sbjct:  119  ISENIREELNEAAEPWGIEVEDVEIKDIRLPEEIKEAMEAQQ  160 (SEQ ID NO:84)
```

At page 67 please replace Table 5C with the following:

Table 5C. BLAST results for NOV5

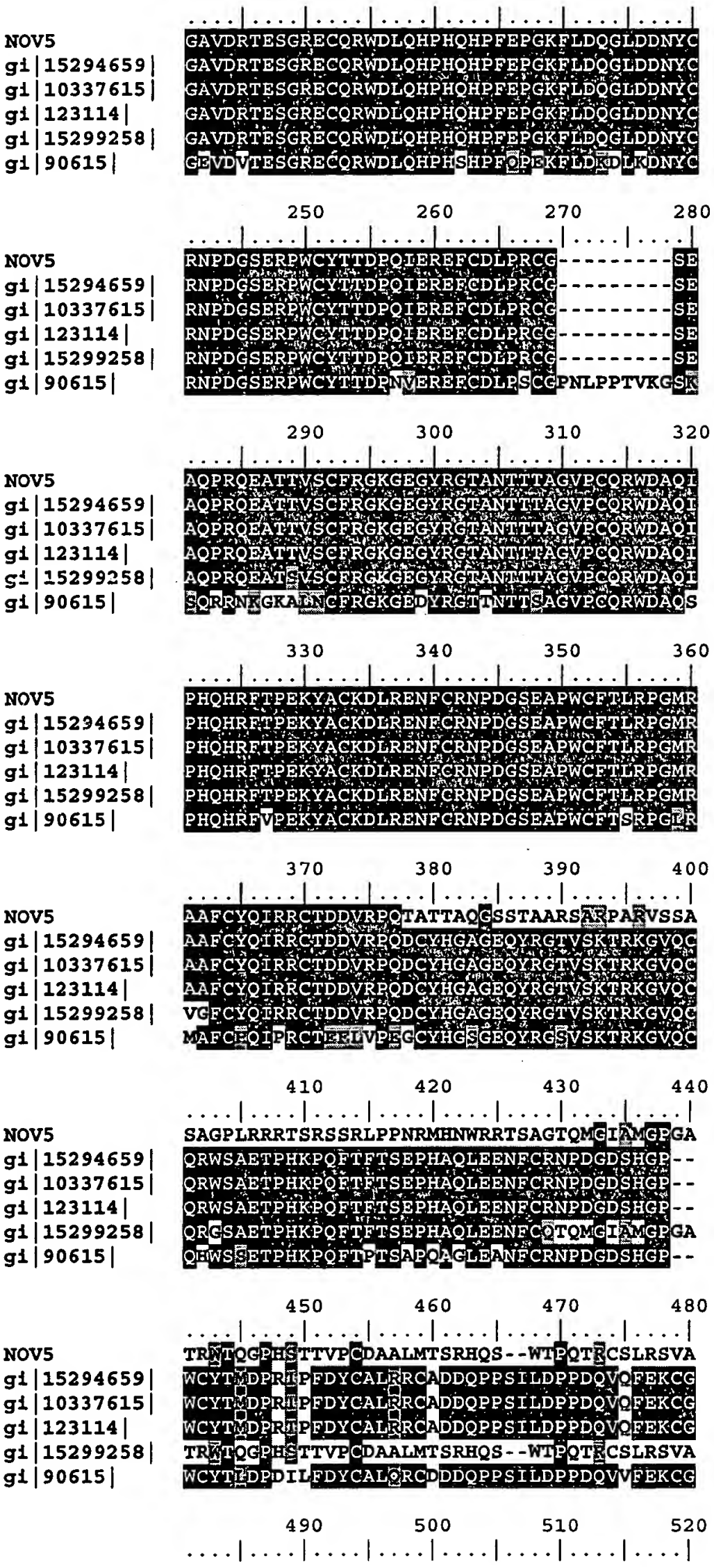
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
~~gi|15294659|ref|XP_054070.1|~~ XP_05407	macrophage stimulating 1 (hepatocyte growth factor-like) [Homo sapiens]	711	561/720 (77%)	577/720 (79%)	0.0
~~gi|10337615|ref|NP_066278.1|~~ NP_066278	macrophage stimulating 1 (hepatocyte growth factor-like) [Homo sapiens]	711	560/720 (77%)	576/720 (79%)	0.0
~~gi|123114|sp|P26927|HGFL_HUMAN~~ P26927	HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN PRECURSOR (MACROPHAGE STIMULATORY PROTEIN) (MSP) (MACROPHAGE STIMULATING PROTEIN)	711	560/720 (77%)	576/720 (79%)	0.0
~~gi|15299258|ref|XP_017811.2|~~ XP_017811	hypothetical protein XP_017811 [Homo sapiens]	529	440/532 (82%)	456/532 (85%)	0.0
~~gi|90615|pir||A40332~~ A40332	macrophage-stimulating protein 1 precursor - mouse	716	449/725 (61%)	507/725 (69%)	0.0

At page 68 please replace Table 5D with the following:

Table 5D Clustal W Sequence Alignment

1) NOV5 (SEQ ID NO:16)
2) ~~gi|15294659|ref|XP_054070.1|~~ **gi|15294659|** XP_05407 macrophage stimulating 1 (hepatocyte growth factor-like) [Homo sapiens] (SEQ ID NO:51)
3) ~~gi|10337615|ref|NP_066278.1|~~ **gi|10337615|** NP_066278 macrophage stimulating 1 (hepatocyte growth factor-like) [Homo sapiens] (SEQ ID NO:52)
4) ~~gi|123114|sp|P26927|HGFL_HUMAN~~ **gi|123114|** P26927HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN PRECURSOR (MACROPHAGE STIMULATORY PROTEIN) (MSP) (MACROPHAGE STIMULATING PROTEIN) (SEQ ID NO:53)
5) ~~gi|15299258|ref|XP_017811.2|~~ **gi|15299258|** XP_017811hypothetical protein XP_017811 [Homo sapiens] (SEQ ID NO:54)
6) ~~gi|90615|pir||A40332~~ **gi|90615|** A40332 macrophage-stimulating protein 1 precursor - mouse (SEQ ID NO:55)

```
                    10        20        30        40
                    ....|....|....|....|....|....|....|....|
NOV5                MGWLPLLLLLTQCLGVPGQRSPLNDFQVLRGTELQHLLHA
gi|15294659|        MGWLPLLLLLTQCLGVPGQRSPLNDFQVLRGTELQHLLHA
gi|10337615|        MGWLPLLLLLTQCLGVPGQRSPLNDFQVLRGTELQHLLHA
gi|123114|          MGWLPLLLLLTQYLGVPGQRSPLNDFQVLRGTELQHLLHA
gi|15299258|        ----------------------------------------
gi|90615|          MGWLPLLLLLVQCSRALGQRSPLNDFQLFRGTELRNLLHT

                    50        60        70        80
                    ....|....|....|....|....|....|....|....|
NOV5                VVPGPWQEDVADAEECAGRCGPLMDCRAFHYNVSSHGCQL
gi|15294659|        VVPGPWQEDVADAEECAGRCGPLMDCRAFHYNVSSHGCQL
gi|10337615|        VVPGPWQEDVADAEECAGRCGPLMDCRAFHYNVSSHGCQL
gi|123114|          VVPGPWQEDVADAEECAGRCGPLMDCRAFHYNVSSHGCQL
gi|15299258|        ----------------------MDCRAFHYNVSSHGCQL
gi|90615|          AVPGPWQEDVADAEECARRCGPLIDCRAFHYNMSSHGCQL

                    90        100       110       120
                    ....|....|....|....|....|....|....|....|
NOV5                LPWTQHSPHTRLRRSGRCDLFQKKDYVRTCIMNNGVGYRG
gi|15294659|        LPWTQHSPHTRLRRSGRCDLFQKKDYVRTCIMNNGVGYRG
gi|10337615|        LPWTQHSPHTRLRRSGRCDLFQKKDYVRTCIMNNGVGYRG
gi|123114|          LPWTQHSPHTRLRRSGRCDLFQKKDYVRTCIMNNGVGYRG
gi|15299258|        LPWTQHSPHTRLRHSGRCDLEQEKDYIRTCIMNNGVGYRG
gi|90615|          LPWTQHSLHTQLYHSSLCHLFQKKDYVRTCIMDNGVSYRG

                    130       140       150       160
                    ....|....|....|....|....|....|....|....|
NOV5                TMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENFCRNP
gi|15294659|        TMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENFCRNP
gi|10337615|        TMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENFCRNP
gi|123114|          TMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENFCRNP
gi|15299258|        TMATTVGGLSCQAWSHKFPNDHQYMPTLRNGLEENFCRNP
gi|90615|          TVARTAGGLPCQAWSRRFPNDHKYTPTPKNGLEENFCRNP

                    170       180       190       200
                    ....|....|....|....|....|....|....|....|
NOV5                DGDPGGPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYR
gi|15294659|        DGDPGGPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYR
gi|10337615|        DGDPGGPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYR
gi|123114|          DGDPGGPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYR
gi|15299258|        DGDPGGPWCHTTDPAVRFQSCGIKSCRVAACVWCNGEEYR
gi|90615|          DGDPRGPWCYTTNRSVRFQSCGIKTCREAVCVLCNGEDYR

                    210       220       230       240
```


NOV5
gi|15294659|
gi|10337615|
gi|123114|
gi|15299258|
gi|90615|
250 260 270 280
290 300 310 320
330 340 350 360
370 380 390 400
410 420 430 440
450 460 470 480
490 500 510 520

```
NOV5              RGWIGWISGVPSCAWLGAIRATHPGQSACGIG--------
gi|15294659|      KRVDRLDQRRSKLRVVGGHPGNSPWTVSLRNRQGQHFCGG
gi|10337615|      KRVDRLDQRRSKLRVVGGHPGNSPWTVSLRNRQGQHFCGG
gi|123114|        KRVDRLDQRRSKLRVVGGHPGNSPWTVSLRNRQGQHFCGG
gi|15299258|      RGWIGWISVVPSCAWLGAIRATHPGQSACGIGQGQHFCGG
gi|90615|         K----RVDKSNKLRVVGGHPGNSPWTVSLRNRQGQHFCGG

                        530       540       550       560
                  ....|....|....|....|....|....|....|....|
NOV5              ----------------MEPLTGYEVWLGTLFQNPQHGE
gi|15294659|      SLVKEQWILTARQCFSSCHMPLTGYEVWLGTLFQNPQHGE
gi|10337615|      SLVKEQWILTARQCFSSCHMPLTGYEVWLGTLFQNPQHGE
gi|123114|        SLVKEQWILTARQCFSSCHMPLTGYEVWLGTLFQNPQHGE
gi|15299258|      SLVKEQWILTARQCFSSCHMPLTGYEVWLGTLFQNPQHGE
gi|90615|         SLVKEQWVLTARQCIWSCHEPLTGYEVWLGTLNQNPQPGE

                        570       580       590       600
                  ....|....|....|....|....|....|....|....|
NOV5              PSLQRVPVAKMVCGPSGSQLVLLKLERSVTLNQRVALICL
gi|15294659|      PSLQRVPVAKMVCGPSGSQLVLLKLERSVTLNQRVALICL
gi|10337615|      PSLQRVPVAKMVCGPSGSQLVLLKLERSVTLNQRVALICL
gi|123114|        PSLQRVPVAKMVCGPSGSQLVLLKLERSVTLNQRVALICL
gi|15299258|      PGLQRVPVAKMLCGPSGSQLVLLKLERSVTLNQRVALICL
gi|90615|         ANLQRVPVAKAVCGPDGSQLVLLKLERPVILNHHVALICL

                        610       620       630       640
                  ....|....|....|....|....|....|....|....|
NOV5              PPEWYVVPPGTKCEIAGWGETKGTGNDTVLNVALLNVISN
gi|15294659|      PPEWYVVPPGTKCEIAGWGETKGTGNDTVLNVALLNVISN
gi|10337615|      PPEWYVVPPGTKCEIAGWGETKGTGNDTVLNVALLNVISN
gi|123114|        PPEWYVVPPGTKCEIAGWGETKGTGNDTVLNVALLNVISN
gi|15299258|      PPE-------------------------------------
gi|90615|         PPEQYVVPPGTKCEIAGWGESIGTSNNTVLEVASVNVISN

                        650       660       670       680
                  ....|....|....|....|....|....|....|....|
NOV5              QECNIKHRG-------------------RGDYGGPLACFT
gi|15294659|      QECNIKHRGRVRESEMCTEGLLAPVGACEGDYGGPLACFT
gi|10337615|      QECNIKHRGRVRESEMCTEGLLAPVGACEGDYGGPLACFT
gi|123114|        QECNIKHRGRVRESEMCTEGLLAPVGACEGDYGGPLACFT
gi|15299258|      -------------------------------------
gi|90615|         QECNTKYRGHIQESEICTQGLVVPVGACEGDYGGPLACYT

                        690       700       710       720
                  ....|....|....|....|....|....|....|....|
NOV5              HNCWVLEGIIIPNRVCARSCWPAVFTRVSVFVDWIHKVMR
gi|15294659|      HNCWVLEGIIIPNRVCARSRWPAVFTRVSVFVDWIHKVMR
gi|10337615|      HNCWVLEGIIIPNRVCARSRWPAVFTRVSVFVDWIHKVMR
gi|123114|        HNCWVLEGIIIPNRVCARSRWPAVFTRVSVFVDWIHKVMR
gi|15299258|      -------------------------------------
gi|90615|         HDCWVLQGLIIPNRVCARPRWPATFTRVSVFVDWINKVMQ

                  ..
NOV5              LG (SEQ ID NO:16)
gi|15294659|      LG (SEQ ID NO:51)
gi|10337615|      LG (SEQ ID NO:52)
gi|123114|        LG (SEQ ID NO:53)
gi|15299258|      -- (SEQ ID NO:54)
gi|90615|         LE (SEQ ID NO:55)
```

At pages 70, please replace Table 5E with the following:

Table 5E. Domain Analysis of NOV5

~~gnl|Pfam|pfam00051~~, kringle, Kringle domain. Kringle domains have been found in plasminogen, hepatocyte growth factors, prothrombin, and apolipoprotein A. Structure is disulfide-rich, nearly all-beta. (SEQ ID NO:85)
CD-Length = 79 residues, 100.0% aligned
Score = 117 bits (292), Expect = 3e-27

```
Query:  191  CVWCNGEEYRGAVDRTESGRECQRWDLQHPHQHPF-EPGKFLDQGLDDNYCRNPDGSERP  249
             |   ||| |||    ||||  ||||| | ||+|    | ++  +|| +|||||||| |||
Sbjct:  1    CYHGNGENYRGTASTTESGAPCQRWDSQTPHRHSKYTPERYPAKGLGENYCRNPDGDERP  60

Query:  250  WCYTTDPQIEREFCDLPRC  268  (of SEQ ID NO:16)
             |||||||++  |+||+|||
Sbjct:  61   WCYTTDPRVRWEYCDIPRC  79  (SEQ ID NO:85)
```

At pages 71, please replace Table 5F, with the following:

Table 5F. Domain Analysis of NOV5

~~gnl|Pfam|pfam00051,~~ kringle, Kringle domain. Kringle domains have been found in plasminogen, hepatocyte growth factors, prothrombin, and apolipoprotein A. Structure is disulfide-rich, nearly all-beta. (SEQ ID NO:85)
CD-Length = 79 residues, 100.0% aligned
Score = 112 bits (279), Expect = 9e-26

```
Query:  283  CFRGKGEGYRGTANTTTAGVPCQRWDAQIPHQHRF-TPEKYACKDLRENFCRNPDGSEAP  341
             |+ | || |||||+|| +| ||||||+| ||+|   |||+|  | | ||+||||||| | |
Sbjct:  1    CYHGNGENYRGTASTTESGAPCQRWDSQTPHRHSKYTPERYPAKGLGENYCRNPDGDERP  60

Query:  342  WCFTLRPGMRAAFCYQIRRC  361  (of SEQ ID NO:16)
             ||+|  | +|  +|  | ||
Sbjct:  61   WCYTTDPRVRWEYC-DIPRC  79  (SEQ ID NO:85)
```

At pages 71, please replace Table 5G with the following:

Table 5G. Domain Analysis of NOV5

~~gnl|Pfam|pfam00051,~~ kringle, Kringle domain. Kringle domains have been found in plasminogen, hepatocyte growth factors, prothrombin, and apolipoprotein A. Structure is disulfide-rich, nearly all-beta. (SEQ ID NO:85)
CD-Length = 79 residues, 100.0% aligned
Score = 104 bits (259), Expect = 2e-23

```
Query:  110  CIMNNGVGYRGTMATTVGGLPCQAWSHKFPNDH-KYTPT--LRNGLEENFCRNPDGDPGG  166
             |   ||  |||| +||  | ||| |  + |+ | ||||      || ||+|||||||
Sbjct:  1    CYHGNGENYRGTASTTESGAPCQRWDSQTPHRHSKYTPERYPAKGLGENYCRNPDGDE-R  59

Query:  167  PWCYTTDPAVRFQSCGIKSC  186  (of SEQ ID NO:16)
             ||||||||  ||++ | |  |
Sbjct:  60   PWCYTTDPRVRWEYCDIPRC  79  (SEQ ID NO:79)
```

At pages 71-72, please replace Table 5H with the following:

Table 5H. Domain Analysis of NOV5

~~gnl|Smart|smart00130,~~ KR, Kringle domain; Named after a Danish pastry. Found in several serine proteases and in ROR-like receptors. Can occur in up to 38 copies (in apolipoprotein(a)). Plasminogen-like kringles possess affinity for free lysine and lysine- containing peptides. (SEQ ID NO:86)
CD-Length = 83 residues, 97.6% aligned
Score = 111 bits (278), Expect = 1e-25

```
Query:  191  CVWCNGEEYRGAVDRTESGRECQRWDLQHPHQHPFEPGKFLDQGLDDNYCRNPDG-SERP  249
             |   ||| |||    |+||+ ||||| | || | | | +| + ||+ |||||||| || |
Sbjct:  3    CYAGNGESYRGTASTTKSGKPCQRWDSQTPHLHRFTPERFPELGLEHNYCRNPDGDSEGP  62

Query:  250  WCYTTDPQIEREFCDLPRCGS  270  (of SEQ ID NO:16)
             ||||||| +  |+||+|+| |
Sbjct:  63   WCYTTDPNVRWEYCDIPQCES  83  (SEQ ID NO:  )
```

At pages 72, please replace Table 5I with the following:

Table 5I. Domain Analysis of NOV5

~~gnl|Smart|smart00130,~~ KR, Kringle domain; Named after a Danish pastry. Found in several serine proteases and in ROR-like receptors. Can occur in up to 38 copies (in apolipoprotein(a)). Plasminogen-like kringles possess affinity for free lysine and lysine- containing peptides.
(SEQ ID NO:86)
CD-Length = 83 residues, 97.6% aligned
Score = 106 bits (265), Expect = 4e-24

```
Query:  108  RTCIMNNGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRN--GLEENFCRNPDGDPG  165
             | |   ||  |||| +||  | ||| |  + |+ |++||       ||| |+|||||||
Sbjct:  1    RDCYAGNGESYRGTASTTKSGKPCQRWDSQTPHLHRFTPERFPELGLEHNYCRNPDGDSE  60

Query:  166  GPWCYTTDPAVRFQSCGIKSC  186  (of SEQ ID NO:16)
             |||||||||  ||++ | |  |
Sbjct:  61   GPWCYTTDPNVRWEYCDIPQC  81  (SEQ ID NO:86)
```

At pages 72, please replace Table 5Jwith the following:

Table 5J. Domain Analysis of NOV5

~~gnl|Smart|smart00130,~~ KR, Kringle domain; Named after a Danish pastry. Found in several serine proteases and in ROR-like receptors. Can occur in up to 38 copies (in apolipoprotein(a)). Plasminogen-like kringles possess affinity for free lysine and lysine- containing peptides.
(SEQ ID NO:86)
CD-Length = 83 residues, 97.6% aligned
Score = 104 bits (260), Expect = 1e-23

```
Query:  283  CFRGKGEGYRGTANTTTAGVPCQRWDAQIPHQHRFTPEKYACKDLRENFCRNPDG-SEAP  341
             |+ | || |||||+|| +| |||||||+| || |||||||++    |   |+|||||| || |
Sbjct:  3    CYAGNGESYRGTASTTKSGKPCQRWDSQTPHLHRFTPERFPELGLEHNYCRNPDGDSEGP  62

Query:  342  WCFTLRPGMRAAFCYQIRRCTD  363  (of SEQ ID NO:16)
             ||+|   | +|  +|   | +|
Sbjct:  63   WCYTTDPNVRWEYCD-IPQCES  83  (SEQ ID NO:86)
```

At pages 72-73, please replace Table 5K with the following:

Table 5K. Domain Analysis of NOV5

~~gnl|Smart|smart00020,~~ Tryp_SPc, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues. (SEQ ID NO:87)
CD-Length = 230 residues, 79.1% aligned
Score = 110 bits (274), Expect = 3e-25

```
Query:  504  PLTGYEVWLGTLFQNPQHGEPSLQRVPVAKMVCGPSGSQ------LVLLKLERSVTLNQR  557
Sbjct:  49   APSSIRVRLGSHDLSSGEET---QTVKVSKVIVHPNYNPSTYDNDIALLKLSEPVTLSDT  105

Query:  558  VALICLPPEWYVVPPGTKCEIAGWGETKGTG--NDTVLNVALLNVISNQECNIKHRGR--  613
Sbjct:  106  VRPICLPSSGYNVPAGTTCTVSGWGRTSESSGSLPDTLQEVNVPIVSNATCRRAYSGGPA  165

Query:  614  -------------------GDYGGPLACFTHNCWVLEGIIIPNRV-CARSCWPAVFTRVS  653
Sbjct:  166  ITDNMLCAGGLEGGKDACQGDSGGPLVC-NDPRWVLVGIVSWGSYGCARPNKPGVYTRVS  224

Query:  654  VFVDWI  659  (of SEQ ID NO:16)
Sbjct:  225  SYLDWI  230  (SEQ ID NO:87)
```

At pages 73, please replace 5L with the following:

Table 5L. Domain Analysis of NOV5

~~gnl|Pfam|pfam00089,~~ trypsin, Trypsin. Proteins recognized include all proteins in families S1, S2A, S2B, S2C, and S5 in the classification of peptidases. Also included are proteins that are clearly members, but that lack peptidase activity, such as haptoglobin and protein Z (PRTZ*). (SEQ ID NO:88)
CD-Length = 217 residues, 77.9% aligned
Score = 92.0 bits (227), Expect = 9e-20

```
Query:  508  YEVWLGTLFQNPQHGEPSLQRVPVAKMV----CGPSGSQLVLLKLERSVTLNQRVALICL  563
Sbjct:  49   VRVVLGE--HNLGTTEGTEQKFDVKKIIVHPNYNPDTNDIALLKLKSPVTLGDTVRPICL  106

Query:  564  PPEWYVVPPGTKCEIAGWGETKGTGNDTVLNVALLNVISNQECNIKHRG-----------  612
Sbjct:  107  PSASSDLPVGTTCSVSGWGRTKNLGTSDTLQEVVVPIVSRETCRSAYGGTVTDTMICAGA  166

Query:  613  -------RGDYGGPLACFTHNCWVLEGIIIPNRVCARSCWPAVFTRVSVFVDWI  659
Sbjct:  167  LGGKDACQGDSGGPLVCSDG---ELVGIVSWGYGCAVGNYPGVYTRVSRYLDWI  217
```

Query: (of SEQ ID NO:16)
Sbjct: (SEQ ID NO:88)

At pages 73, please replace Table 5M with the following:

Table 5M. Domain Analysis of NOV5

~~gnl|Smart|smart00473,~~ PAN_AP, divergent subfamily of APPLE domains; Apple-like domains present in Plasminogen, C. elegans hypothetical ORFs and the extracellular portion of plant receptor-like protein kinases. Predicted to possess protein- and/or carbohydrate-binding functions. (SEQ ID NO:89)
CD-Length = 79 residues, 94.9% aligned
Score = 52.0 bits (123), Expect = 1e-07

```
Query:  25   DFQVLRGTELQHLLHAVVPGPWQEDVADAEECAGRC-GPLMDCRAFHYNVSSHGCQLLPW  83
             |  |  |+|           |    ||  |||| +|       ||+| ||  + || |
Sbjct:  5    CFVRLPNTKL------PDFSPIVISVASLEECAQKCLNSNCSCRSFTYNNDTKGCLLWSE  58

Query:  84   TQHSPHTRLRRSGRCDLFQKK  104  (of SEQ ID NO:16)
             +      +|  ||  | ++|
Sbjct:  59   SSLGDARQLLPSGGVDYYEKI  79   (SEQ ID NO:89)
```

At pages 74, please replace Table 5N with the following:

Table 5N. Domain Analysis of NOV5

~~gnl|Pfam|pfam00024,~~ PAN, PAN domain. The PAN domain contains a conserved core of three disulphide bridges. In some members of the family there is an additional fourth disulphide bridge the links the N and C termini of the domain. The domain is found in diverse proteins, in some they mediate protein-protein interactions, in others they mediate protein-carbohydrate interactions. (SEQ ID NO:159)
CD-Length = 78 residues, 76.9% aligned
Score = 50.1 bits (118), Expect = 4e-07

```
Query:  45   PWQEDVADAEECAGRCGPLMD-CRAFHYNVSSHGCQLLPWTQHSPHTRLRRSGRCDLFQK  103
                +|   ||||  |      ||+| ||  |  | |   +  |     | | + | ++|
Sbjct:  17   ISVVNVPSLEECAALCLEEPRVCRSFTYNNKSKQCLLKSESSGSLPRLKRPSQKVDYYEK
```

Query: (of SEQ ID NO:16)

Sbjct: (SEQ ID NO:159)

At page 78 please replace Table 6C with the following:

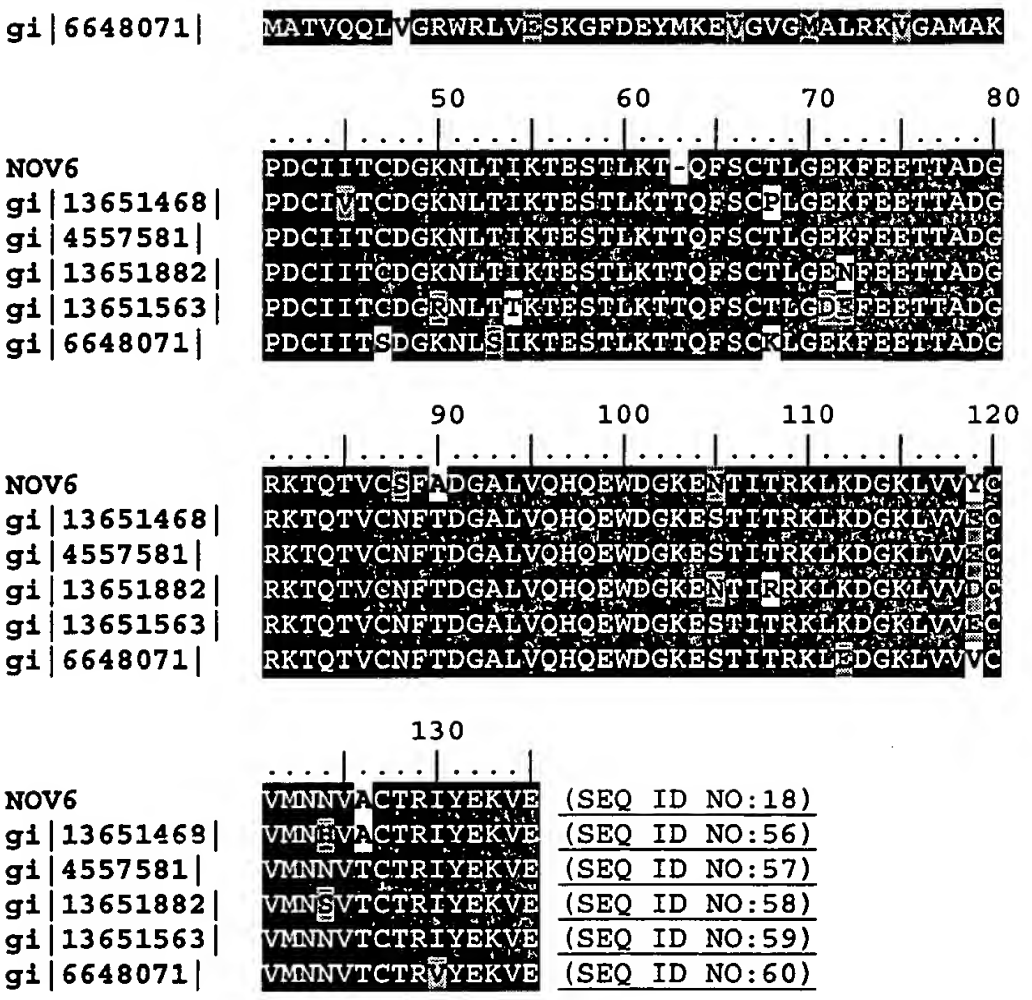
Table 6C. BLAST results for NOV6

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
~~gi|13651468|ref|XP 016351.1|~~ XP 016351	similar to GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-BR) (H. sapiens) [Homo sapiens]	135	122/135 (90%)	126/135 (92%)	1e-58
~~gi|4557581|ref|NP 001435.1|~~ NP 001435	fatty acid binding protein 5 (psoriasis-associated); E-FABP [Homo sapiens]	135	124/135 (91%)	126/135 (92%)	1e-58
~~gi|13651882|ref|XP 011655.5|~~ XP 011655	fatty acid binding protein 5 (psoriasis-associated) [Homo sapiens]	135	119/135 (88%)	124/135 (91%)	6e-57
~~gi|13651563|ref|XP 015760.1|~~ XP 015760	similar to GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-BR) (H. sapiens) [Homo sapiens]	135	118/135 (87%)	125/135 (92%)	5e-56
~~gi|6648071|sp|P55052|FABE BOVIN~~ P55052	FATTY ACID-BINDING PROTEIN, EPIDERMAL (E-FABP)	135	117/135 (86%)	124/135 (91%)	1e-55

At page 79 please replace Table 6D with the following:

Table 6D Information for the ClustalW proteins

1) NOV6 (SEQ ID NO:18)
2) ~~gi|13651468|ref|XP 016351.1|~~ **gi|13651468|** XP 016351similar to GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-BR) (H. sapiens) [Homo sapiens] (SEQ ID NO:56)
3) ~~gi|4557581|ref|NP 001435.1|~~ **gi|4557581|** NP 001435fatty acid binding protein 5 (psoriasis-associated); E-FABP [Homo sapiens] (SEQ ID NO:57)
4) ~~gi|13651882|ref|XP 011655.5|~~ **gi|13651882|** XP 011655fatty acid binding protein 5 (psoriasis-associated) [Homo sapiens] (SEQ ID NO:58)
5) ~~gi|13651563|ref|XP 015760.1|~~ **gi|13651563|** XP 015760similar to GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-BR) (H. sapiens) [Homo sapiens] (SEQ ID NO:59)
6) ~~gi|6648071|sp|P55052|FABE BOVIN~~ **gi|13651563|** P55052 FATTY ACID-BINDING PROTEIN, EPIDERMAL (E-FABP) (SEQ ID NO:60)



Page 80, please replace Table 6E with the following:

Table 6E. Domain Analysis of NOV6

~~gnl|Pfam|pfam00061,~~ lipocalin, Lipocalin / cytosolic fatty-acid binding protein family. Lipocalins are transporters for small hydrophobic molecules, such as lipids, steroid hormones, bilins, and retinoids. Alignment subsumes both the lipocalin and fatty acid binding protein signatures from PROSITE. This is supported on structural and functional grounds. Structure is an eight-stranded beta barrel. (SEQ ID NO:90)
CD-Length = 145 residues, 76.6% aligned
Score = 53.1 bits (126), Expect = 1e-08

```
Query:  9    GRWRLVDSKRFDEYMK-EGGVGTALRKMDAMAK-PDCIITCDGKNLTIKTESTLKTQFSC  66
             |+| || |  ||  +| | ||  | ||     |  +  |  ||     |  |+  | + +
Sbjct:  4    GKWYLVASANFDPELKEELGVLEATRKEITPLKEGNLEIVFDGDKNGICEETFGKLEKTK  63

Query:  67   TLGEKFEETTADGRKTQTVCSFADGALVQHQEWDGKENTITRKLKDGKLVV  117
              || +|+  | | |       + +  ||  |+ || | + | +|      +
Sbjct:  64   KLGVEFDYYTGDNRFVVLDTDYDNYLLVCVQKGDGNETSRTAELYGRTPEL  114
```

Query: (of SEQ ID NO:18)

Sbjct: (SEQ ID NO:90)

At page 84 please replace Table 7C with the following:

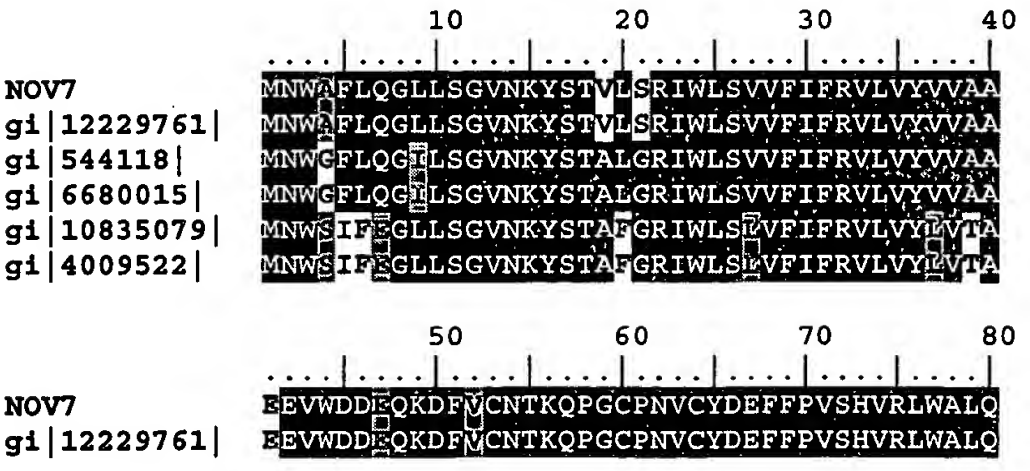
Table 7C. BLAST results for NOV7

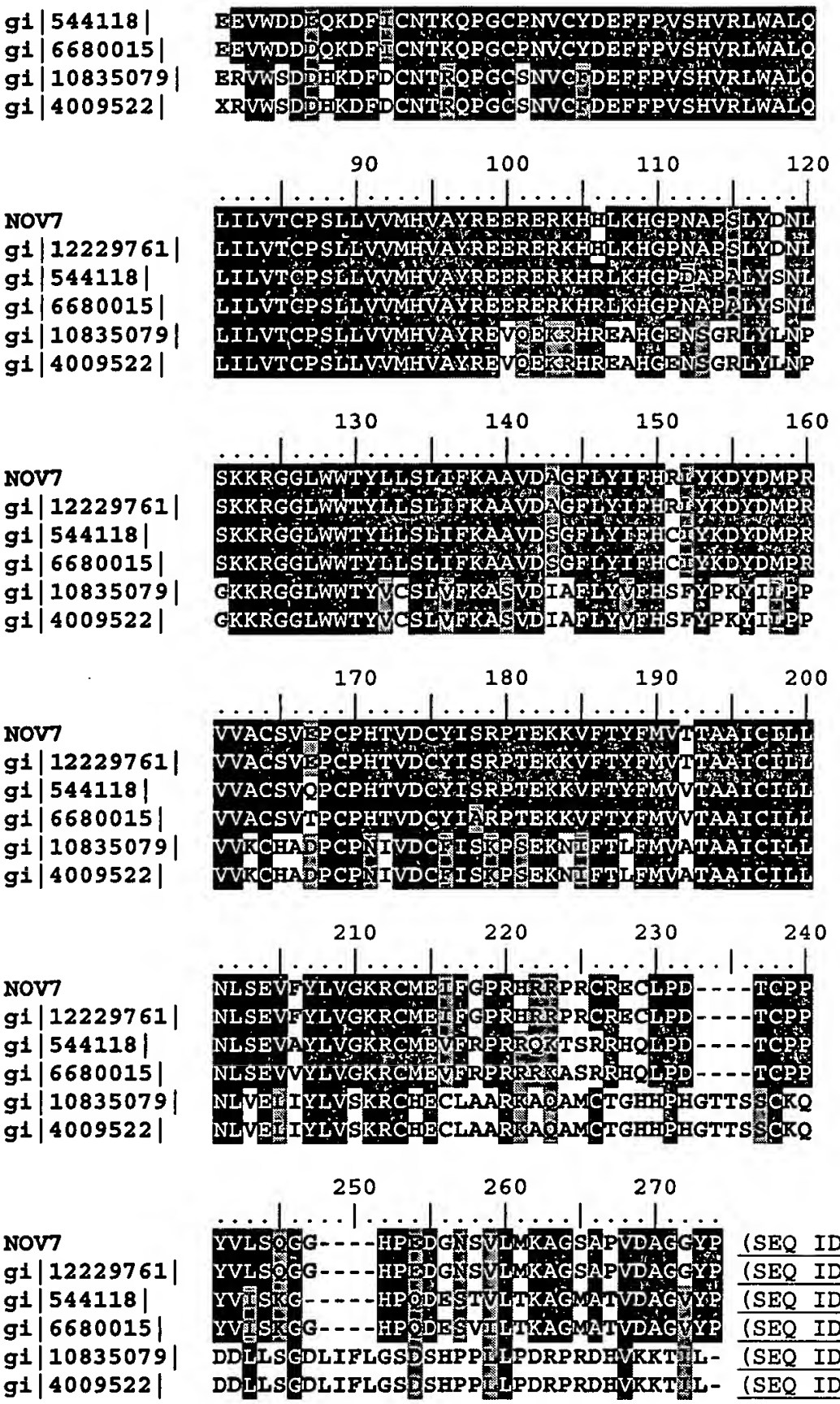
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
~~gi|12229761|sp|Q9NTQ9|CXB4_HUMAN~~ Q9NTQ9	GAP JUNCTION BETA-4 PROTEIN (CONNEXIN 30.3) (CX30.3)	266	266/266 (100%)	266/266 (100%)	e-155
~~gi|544118|sp|P36380|CXB5_RAT~~ P36380	GAP JUNCTION BETA-5 PROTEIN (CONNEXIN 30.3) (CX30.3)	265	230/266 (86%)	245/266 (91%)	e-132
~~gi|6680015|ref|NP_032153.1|~~ NP_032153	gap junction membrane channel protein beta 4; connexin 30.3 [Mus musculus]	266	230/266 (86%)	244/266 (91%)	e-131
~~gi|10835079|ref|NP_005259.1|~~ NP_05259	gap junction protein, beta 5 (connexin 31.1) [Homo sapiens]	273	153/226 (67%)	177/226 (77%)	3e-88
~~gi|4009522|gb|AAC95472.1|~~ (AF099731)AAC95472	connexin 31.1 [Homo sapiens]	273	152/226 (67%)	176/226 (77%)	1e-87

At page 85 please replace Table 7D with the following:

Table 7D. Information for the ClustalW proteins

1) NOV7 (SEQ ID NO:20)
2) ~~gi|12229761|sp|Q9NTQ9|CXB4_HUMAN~~ Q9NTQ9 GAP JUNCTION BETA-4 PROTEIN (CONNEXIN 30.3) (CX30.3) (SEQ ID NO:61)
3) ~~gi|544118|sp|P36380|CXB5_RAT~~ Q9NTQ9 GAP JUNCTION BETA-5 PROTEIN (CONNEXIN 30.3) (CX30.3) (SEQ ID NO:62)
4) ~~gi|6680015|ref|NP_032153.1|~~ NP_032153gap junction membrane channel protein beta 4; connexin 30.3 [Mus musculus] (SEQ ID NO:63)
5) ~~gi|10835079|ref|NP_005259.1|~~ NP_05259 gap junction protein, beta 5 (connexin 31.1) [Homo sapiens] (SEQ ID NO:64)
6) ~~gi|4009522|gb|AAC95472.1|~~ AAC95472 (AF099731) connexin 31.1 [Homo sapiens] (SEQ ID NO:65)





At page 86 please replace Table 7E with the following:

Table 7E. Domain Analysis of NOV7

~~gnl|Pfam|pfam00029,~~ connexin, Connexin. (SEQ ID NO:91)
CD-Length = 218 residues, 100.0% aligned
Score = 318 bits (814), Expect = 3e-88

```
Query:  1    MNWAFLQGLLSGVNKYSTVLSRIWLSVVFIFRVLVYVVAAEEVWDDEQKDFVCNTKQPGC  60
             |+|+||  || ||||+|| + +|||||+||||+||  |||| || ||| ||||||+||||
Sbjct:  1    MDWSFLGRLLEGVNKHSTAIGKIWLSVLFIFRILVLGVAAESVWGDEQSDFVCNTQQPGC  60

Query:  61   PNVCYDEFFPVSHVRLWALQLILVTCPSLLVVMHVAYREERERKHHLKHGPNAPSLYDNL  120
              |||||+|||+|||||| |||| |+ |||| + |||||  || |   |   ++  ||
Sbjct:  61   ENVCYDQFFPISHVRLWVLQLIFVSTPSLLYLGHVAYRVRREEKLREKEEEHSKGLYSEE  120

Query:  121  SKK-----------RGGLWWTYLLSLIFKAAVDAGFLYIFHRLYKDYDMPRVVACSVEPC  169
             +||           ||||||||+ |+|||+  + ||||  + ||  + |  +| ||  ||
Sbjct:  121  AKKRCGSEDGKVRIRGGLWWTYVFSIIFKSIFEVGFLYGQYLLY-GFTMSPLVVCSRAPC  179

Query:  170  PHTVDCYISRPTEKKVFTYFMVTTAAICILLNLSEVFYL  208  (of SEQ ID NO:20)
             ||||||++||||||  +|  ||+  +|||+||||+|+|||
Sbjct:  180  PHTVDCFVSRPTEKTIFIVFMLVVSAICLLLNLAELFYL  218  (SEQ ID NO:91)
```

At page 87, please replace Table 7F with the following:

Table 7F. Domain Analysis of NOV7

~~gnl|Smart|smart00037,~~ CNX, Connexin homologues; Connexin channels participate in the regulation of signaling between developing and differentiated cell types. (SEQ ID NO:160)
CD-Length = 34 residues, 100.0% aligned
Score = 79.0 bits (193), Expect = 3e-16

```
Query:  42   EVWDDEQKDFVCNTKQPGCPNVCYDEFFPVSHVR  75  (of SEQ ID NO:20)
              || ||| || |||+|||| |||||+|||+||||
Sbjct:  1    SVWGDEQSDFTCNTQQPGCENVCYDQFFPISHVR  34  (SEQ ID NO:160)
```

At page 100, please replace Table 9C with the following:

Table 9C. BLAST results for NOV9

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
~~gi|13591536|emb|CAC 36351.1|~~ CAC36351 (AL109613)	dJ1033H22.1 (KIAA0554 protein) [Homo sapiens]	434	373/430 (86%)	375/430 (86%)	0.0

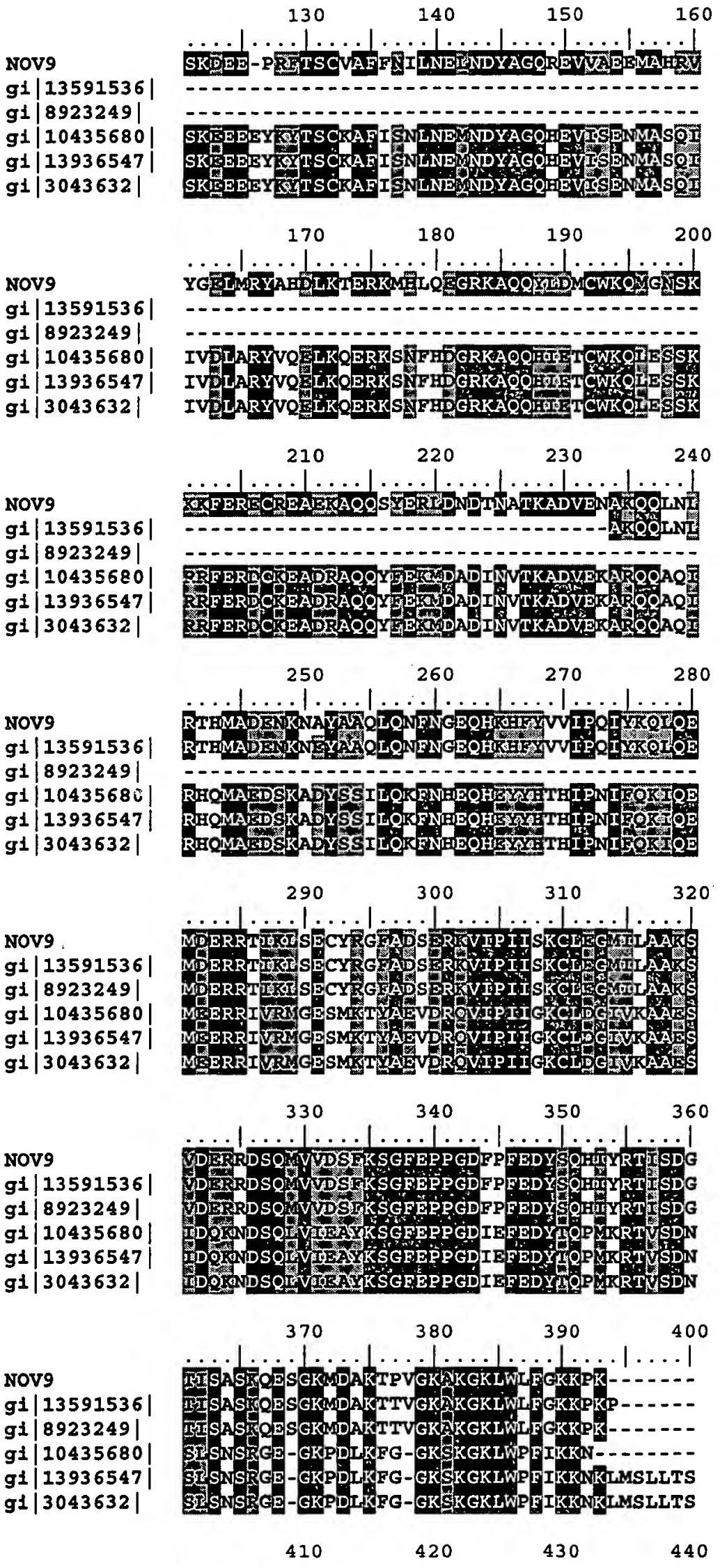
~~gi|8923249|ref|NP_060207.1|~~ NP_060207	hypothetical protein FLJ20275 [Homo sapiens]	330	328/330 (99%)	329/330 (99%)	e-175
~~gi|10435680|dbj|BAB14638.1|~~ BAB14638 (AK023681)	unnamed protein product [Homo sapiens]	592	319/595 (53%)	432/595 (71%)	e-160
~~gi|13936547|gb|AAK49824.1|AF265550_1~~ AAK49824 (AF265550)	formin-binding protein 17 [Homo sapiens]	679	307/624 (49%)	422/624 (67%)	e-148
~~gi|3043632|dbj|BAA25480.1|~~ BAA25480 (AB011126)	KIAA0554 protein [Homo sapiens]	674	307/624 (49%)	422/624 (67%)	e-148

At page 100 please replace Table 9D with the following:

Table 9D. ClustalW Analysis of NOV9

1) Novel NOV9 (SEQ ID NO:24)
3) ~~gi\|13591536\|emb\|CAC36351.1\|~~ CAC36351 **gi\|13591536\|** (AL109613) dJ1033H22.1 (KIAA0554 protein) [Homo sapiens] (SEQ ID NO:66)
4) ~~gi\|8923249\|ref\|NP_060207.1\|~~ NP_060207 **gi\|8923249\|** hypothetical protein FLJ20275 [Homo sapiens] (SEQ ID NO:67)
5) ~~gi\|10435680\|dbj\|BAB14638.1\|~~ BAB14638 **gi\|10435680\|** (AK023681) unnamed protein product [Homo sapiens] (SEQ ID NO:68)
6) ~~gi\|13936547\|gb\|AAK49824.1\|AF265550_1~~ AAK49824 **gi\|13936547\|** (AF265550) formin-binding protein 17 [Homo sapiens] (SEQ ID NO:69)
7) ~~gi\|3043632\|dbj\|BAA25480.1\|~~ BAA25480 **gi\|3043632\|** (AB011126) KIAA0554 protein [Homo sapiens] (SEQ ID NO:70)

```
                        10        20        30        40
                ....|....|....|....|....|....|....|....|
NOV9            ----------------------------------------
gi|13591536|    ----------------------------------------
gi|8923249|     ----------------------------------------
gi|10435680|    ----------------------------------------
gi|13936547|    LWNGGEEEPPRRPRARSCEPEEAARTPGFPPSRGSRGAKG
gi|3043632|     -----EEEPPRRPRARSCEPEEAARTPGFPPSRGSRGAKG

                        50        60        70        80
                ....|....|....|....|....|....|....|....|
NOV9            ----------------------MSWGTELWDQFDSLQKHT
gi|13591536|    ----------------------------------------
gi|8923249|     ----------------------------------------
gi|10435680|    ----------------------MSWGTELWDQFDNLEKHT
gi|13936547|    SPGRGTREPRPPRGAPLRVPCTMSWGTELWDQFDNLEKHT
gi|3043632|     SPGRGTREPRPPRGAPLRVPCTMSWGTELWDQFDNLEKHT

                        90        100       110       120
                ....|....|....|....|....|....|....|....|
NOV9            QWGIDFLERYAKFVKERIEIEQNYAKQLRNLVKKYCPKRS
gi|13591536|    ----------------------------------------
gi|8923249|     ----------------------------------------
gi|10435680|    QWGIDILEKYIKFVKERTEIELSYAKQLRNLSKKYQPKKN
gi|13936547|    QWGIDILEKYIKFVKERTEIELSYAKQLRNLSKKYQPKKN
gi|3043632|     QWGIDILEKYIKFVKERTEIELSYAKQLRNLSKKYQPKKN
```


130 140 150 160
NOV9
gi|13591536|
gi|8923249|
gi|10435680|
gi|13936547|
gi|3043632|
170 180 190 200
NOV9
gi|13591536|
gi|8923249|
gi|10435680|
gi|13936547|
gi|3043632|
210 220 230 240
NOV9
gi|13591536|
gi|8923249|
gi|10435680|
gi|13936547|
gi|3043632|
250 260 270 280
NOV9
gi|13591536|
gi|8923249|
gi|10435680|
gi|13936547|
gi|3043632|
290 300 310 320
NOV9
gi|13591536|
gi|8923249|
gi|10435680|
gi|13936547|
gi|3043632|
330 340 350 360
NOV9
gi|13591536|
gi|8923249|
gi|10435680|
gi|13936547|
gi|3043632|
370 380 390 400
NOV9
gi|13591536|
gi|8923249|
gi|10435680|
gi|13936547|
gi|3043632|
410 420 430 440

```
                    ....|....|....|....|....|....|....|....|
NOV9                ----------------------------------------
gi|13591536|        --QSPPLTPTSLFTSSTPNGSQFLTFSIEPVHYCMNEIKT
gi|8923249|         ----------------------------------------
gi|10435680|        --------------------KSPKQQKEPLSHRFNEFMT
gi|13936547|        PHQPPPPPPASASPSAVPNGPQSPKQQKEPLSHRFNEFMT
gi|3043632|         PHQPPPPPPASASPSAVPNGPQSPKQQKEPLSHRFNEFMT

                              450       460       470       480
                    ....|....|....|....|....|....|....|....|
NOV9                ------------G------PALEDFSHLPPEQRRKKLQQ
gi|13591536|        GKPRIPSFRSLKRGG-----PALEDFSHLPPEQRRKKLQQ
gi|8923249|         ------------G------PALEDFSHLPPEQRRKKLQQ
gi|10435680|        SKPKIHCFRSLKRGLSLKLGATPEDFSNLPPEQRRKKLQQ
gi|13936547|        SKPKIHCFRSLKRGLSLKLGATPEDFSNLPPEQRRKKLQQ
gi|3043632|         SKPKIHCFRSLKRGLSLKLGATPEDFSNLPPEQRRKKLQQ

                              490       500       510       520
                    ....|....|....|....|....|....|....|....|
NOV9                RIDELNRELQKESDQKDALNKMKDVYEKDPQMGDPGSLQP
gi|13591536|        RIDELNRELQKESDQKDALNKMKDVYEKNPQMGDPGSLQP
gi|8923249|         RIDELNRELQKESDQKDALNKMKDVYEKNPQMGDPGSLQP
gi|10435680|        KVDELNKEIQKEMDQRDALTKMKDVYLKNPQMGDPASLDH
gi|13936547|        KVDELNKEIQKEMDQRDALTKMKDVYLKNPQMGDPASLDH
gi|3043632|         KVDELNKEIQKEMDQRDALTKMKDVYLKNPQMGDPASLDH

                              530       540       550       560
                    ....|....|....|....|....|....|....|....|
NOV9                KLAETMNNIDRLRMEIHKNEAWLSEVEGKTGGRGD--RRH
gi|13591536|        KLAETMNNIDRLRMEIHKNEAWLSEVEGKTGGRGD--RRH
gi|8923249|         KLAETMNNIDRLRMEIHKNEAWLSEVEGKTGGRGD--RRH
gi|10435680|        KLAEVSQNIEKLRVETQKFEAWLAEVEGRLPARNEQARRQ
gi|13936547|        KLAEVSQNIEKLRVETQKFEAWLAEVEGRLPARSEQARRQ
gi|3043632|         KLAEVSQNIEKLRVETQKFEAWLAEVEGRLPARSEQARRQ

                              570       580       590       600
                    ....|....|....|....|....|....|....|....|
NOV9                SSDIN-------HLVTQGRESPEGSYTDDANQEVRGPPQQ
gi|13591536|        SSDIN-------HLVTQGRESPEGSYTDDANQEVRGPPQQ
gi|8923249|         SSDIN-------HLVTQGRESPEGSYTDDANQEVRGPPQQ
gi|10435680|        SGLYDSQNPPTVNNCAQDRESPDGSYTEEQSQESS----EM
gi|13936547|        SGLYDSQNPPTVNNCAQDRESPDGSYTEEQSQESS----EM
gi|3043632|         SGLYDSQNPPTVNNCAQDRESPDGSYTEEQSQESS----EM

                              610       620       630       640
                    ....|....|....|....|....|....|....|....|
NOV9                HGHHNEFDDEFEDDDPLPAIGHCKALYPFDGHNEGTLAMK
gi|13591536|        HGHHNEFDDEFEDDDPLPAIGHCKALYPFDGHNEGTLAMK
gi|8923249|         HGHHNEFDDEFEDDDPLPAIGHCKALYPFDGHNEGTLAMK
gi|10435680|        KVLATDFDDEFDDEEPLPAIGTCKALYTFEGQNEGTISVV
gi|13936547|        KVLATDFDDEFDDEEPLPAIGTCKALYTFEGQNEGTISVV
gi|3043632|         KVLATDFDDEFDDEEPLPAIGTCKALYTFEGQNEGTISVV

                              650       660       670       680
                    ....|....|....|....|....|....|....|....|
NOV9                EGEVLYTIEEDKGDGWTRARRQNGEEGYVPTSYTDVTLEK
gi|13591536|        EGEVLYTIEEDKGDGWTRARRQNGEEGYVPTSYTDVTLEK
gi|8923249|         EGEVLYTIEEDKGDGWTRARRQNGEEGYVPTSYTDVTLEK
gi|10435680|        EGETLYYIEEDKGDGWTRIRRNEDEEGYVPTSYVEVCLDK
gi|13936547|        EGETLYYIEEDKGDGWTRIRRNEDEEGYVPTSYVEVCLDK
gi|3043632|         EGETLYYIEEDKGDGWTRIRRNEDEEGYVPTSYVEVCLDK

                    ....|....
```

NOV9	NSKGS----	(SEQ ID NO:24)
gi|13591536|	NSKGAVTYI	(SEQ ID NO:66)
gi|8923249|	NSKGS----	(SEQ ID NO:67)
gi|10435680|	NAKGAKTYI	(SEQ ID NO:68)
gi|13936547|	NAKDS----	(SEQ ID NO:69)
gi|3043632|	NAKDS----	(SEQ ID NO:70)

At page 103, please replace Table 9E with the following:

Table 9E. Domain Analysis of NOV9

~~gnl\|Smart\|smart00326,~~ SH3, Src homology 3 domains; Src homology 3 (SH3) domains bind to target proteins through sequences containing proline and hydrophobic amino acids. Pro-containing polypeptides may bind to SH3 domains in 2 different binding orientations. (SEQ ID NO:92)
CD-Length = 59 residues, 88.1% aligned
Score = 64.7 bits (156), Expect = 1e-11

```
Query:  484  HCKAIYPFDGHNEGTLAMKEGEVLYIIEEDKGDGWTRARRQNGEEGYVPTSYI  536
             +|+| +   +   |+ |+|+++ ++|+  ||| + |   |+||  |++|+
Sbjct:  4    QVRALYDYTAQDPDELSFKKGDIITVLEKS-DDGWWKGRLGTGKEGLFPSNYV  55
```

Query: (of SEQ ID NO:24)

Sbjct: (SEQ ID NO:92)

At page 104, please replace Table 9F with the following:

Table 9F. Domain Analysis of NOV9

~~gnl\|Pfam\|pfam00018,~~ SH3, SH3 domain. SH3 (Src homology 3) domains are often indicative of a protein involved in signal transduction related to cytoskeletal organization. First described in the Src cytoplasmic tyrosine kinase. The structure is a partly opened beta barrel. (SEQ ID NO:93)
CD-Length = 57 residues, 91.2% aligned
Score = 63.5 bits (153), Expect = 3e-11

```
Query:  486  KAIYPFDGHNEGTLAMKEGEVLYIIEEDKGDGWTRARRQNGEEGYVPTSYID  537
             A+Y +       L+ K+G+++ ++E+    GW + R +  +EG +P++Y+
Sbjct:  4    VALYDYQARESDELSFKKGDIIIVLEKSDDGGWWKGRLKGTKEGLIPSNYVE  55
```

Query: of SEQ ID NO:24)

Sbjct: (SEQ ID NO:93)

At page 104, please replace Table 9 with the following:

Table 9G. Domain Analysis of NOV9

~~gnl|Smart|smart00055,~~ FCH, Fes/CIP4 homology domain; Alignment extended from original report. Highly alpha-helical. Also known as the RAEYL motif or the S. pombe Cdc15 N-terminal domain. (SEQ ID NO:94)
CD-Length = 91 residues, 97.8% aligned
Score = 58.2 bits (139), Expect = 1e-09

```
Query:  1    MSWGTELWDQFDSLDKHTQWGIDFLERYAKFVKERIEIEQNYAKQLRNLVKKYCPKRSSK  60
             | + +||  |  |++|     + |+  ||    ||++|| +||+ |||+|+ |  ||   +
Sbjct:  1    MGFWSELDDGFEALLSRLKNGLRLLEDLKKFMRERAKIEEEYAKKLQKLSKK--LRAVRD  58

Query:  61   DEEPRFTSCVAFFNILNELNDYAGQREVVAE  91  (of SEQ ID NO:24)
              |    +   |+  +|+| +  | |   ++|
Sbjct:  59   TESELGSLRKAWEVLLSETDALAKQHLQLSE  89  (SEQ ID NO:94)
```

At page 104, please replace Table 9H with the following:

Table 9H. Domain Analysis of NOV9

~~gnl|Pfam|pfam00611,~~ FCH, Fes/CIP4 homology domain. Alignment extended from. Highly alpha-helical. (SEQ ID NO:95)
CD-Length = 94 residues, 97.9% aligned
Score = 40.0 bits (92), Expect = 3e-04

```
Query:  1    MSWGTELWDQ-FDSLDKHTQWGIDFLERYAKFVKERIEIEQNYAKQLRNLVKKYCPKRSS  59
             | +|+||  +   +|       +  ||   ||+ || +||+ || +|++|  +     ++
Sbjct:  1    MGFGSELCPEGHKALLSRQDNELRLLEEMKKFMAERAKIEKEYAGKLQHLSAQVGKGPAT  60

Query:  60   KDEEPRFTSCVAFFNILNELNDYAGQREVVAE  91  (of SEQ ID NO:24)
              + |   +|  ++  ||+|    +     ++|
Sbjct:  61   AEGEDELSSLKSWAVILSETEQQSKIHLQISE  92  (SEQ ID NO:95)
```

At page 113 please replace Table 10F with the following:

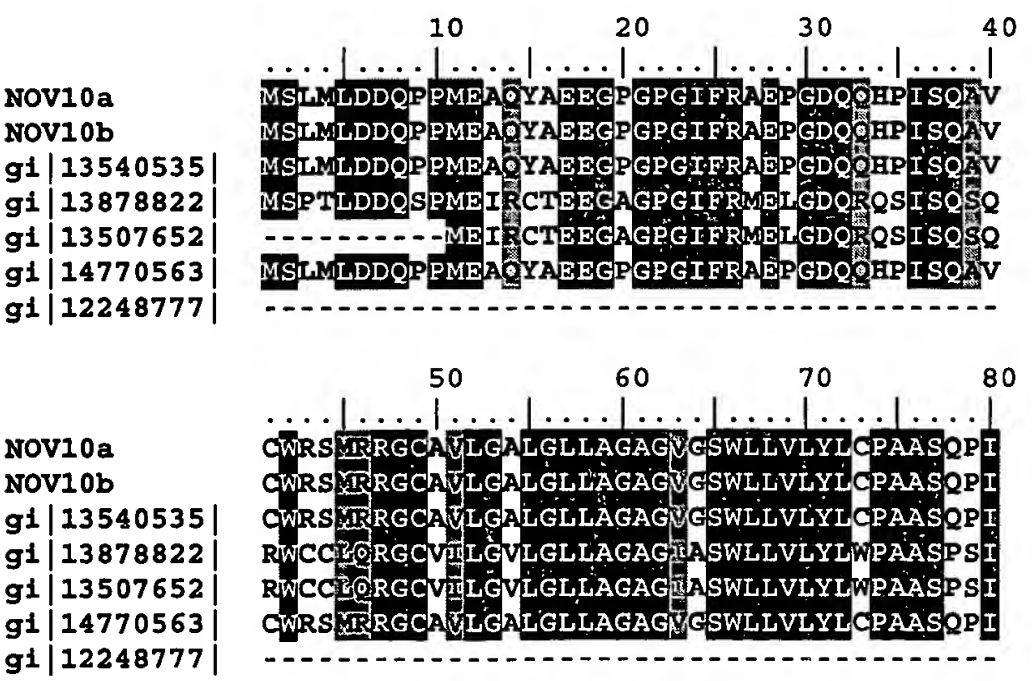
Table 10F. BLAST results for NOV10a

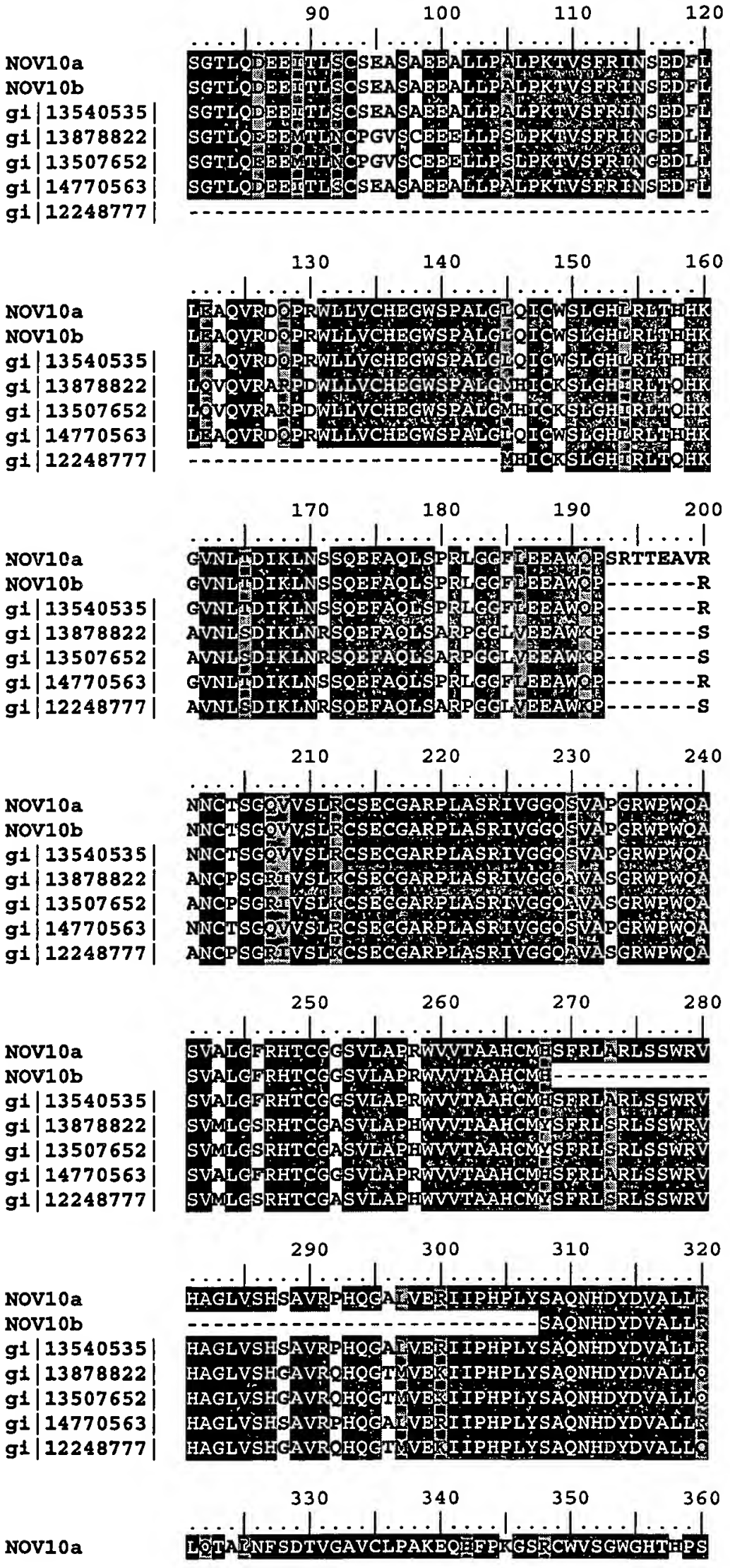
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
~~gi|13540535|ref|NP 110397.1|~~ NP 110397	transmembrane protease, serine 5; spinesin [Homo sapiens]	457	452/463 (97%)	453/463 (97%)	0.0
~~gi|13878822|sp|Q9ER 04|TMS5 MOUSE~~ Q9ER04	TRANSMEMBRANE PROTEASE, SERINE 5 (SPINESIN)	455	360/461 (78%)	394/461 (85%)	0.0
~~gi|13507652|ref|NP 109634.1|~~ NP 109634	transmembrane protease, serine 5 (spinesin) [Mus musculus]	445	354/451 (78%)	388/451 (85%),	0.0
~~gi|14770563|ref|XP 041427.1|~~ XP 041427	transmembrane protease, serine 5 [Homo sapiens]	398	354/362 (97%)	355/362 (97%)	0.0
~~gi|12248777|dbj|BAB 20276.1|~~ BAB20276 (AB016229)	type 2 spinesin [Mus musculus]	311	260/317 (82%)	281/317 (88%)	e-146

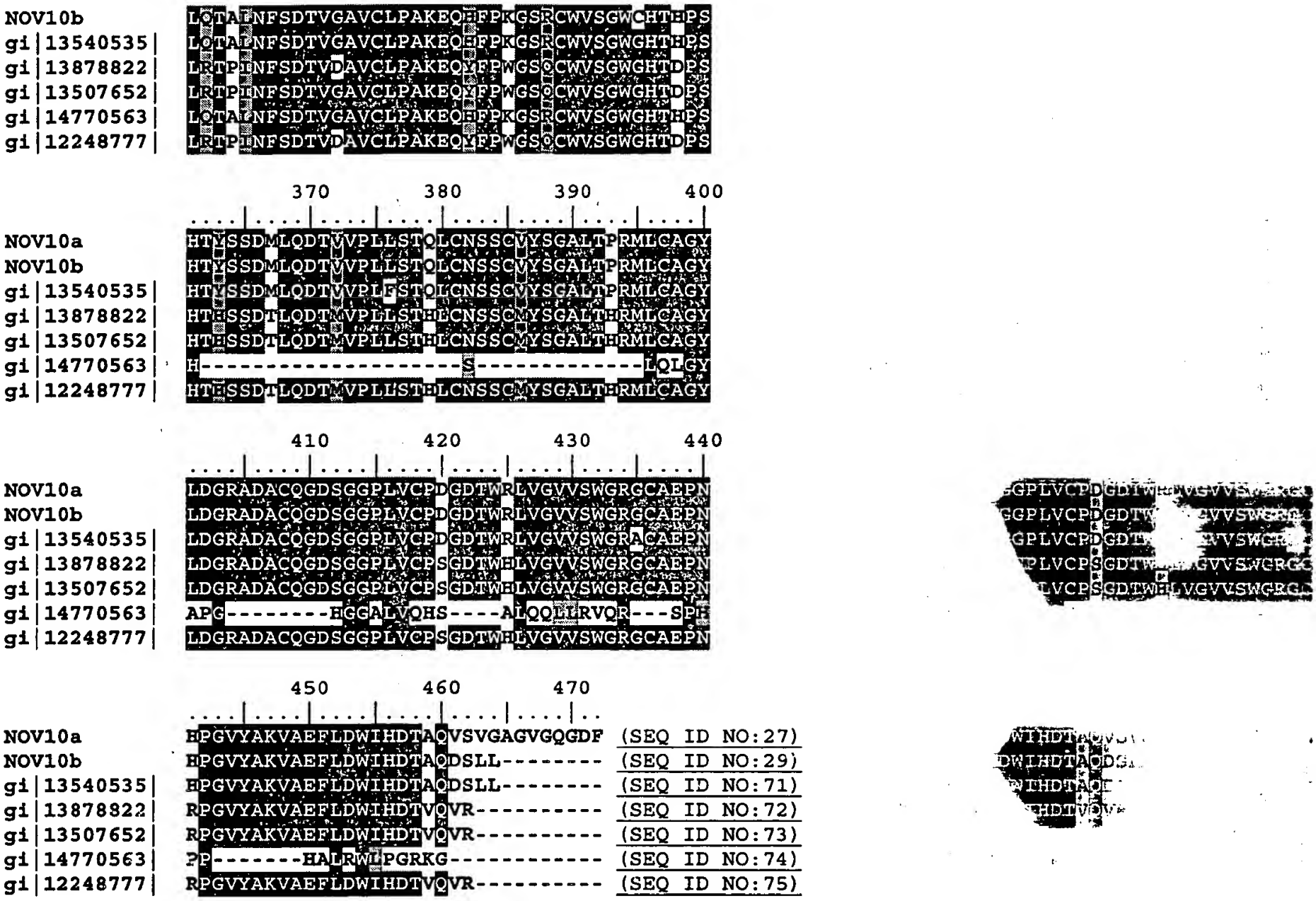
At page 114 please replace Table 10G with the following:

Table 10G. ClustalW Analysis of NOV10

1) Novel NOV10a (SEQ ID NO:27)
2) Novel NOV10b (SEQ ID NO:29)
4) ~~gi|13540535|ref|NP 110397.1|~~ NP 110397 **gi|13540535|** transmembrane protease, serine 5; spinesin [Homo sapiens] (SEQ ID NO:71)
5) ~~gi|13878822|sp|Q9ER04|TMS5 MOUSE~~ Q9ER04 **gi|13878822|** TRANSMEMBRANE PROTEASE, SERINE 5 (SPINESIN) (SEQ ID NO:72)
6) ~~gi|13507652|ref|NP 109634.1|~~ NP 109634 **gi|13507652|** transmembrane protease, serine 5 (spinesin) [Mus musculus] (SEQ ID NO:73)
7) ~~gi|14770563|ref|XP 041427.1|~~ XP 041427 **gi|14770563|** transmembrane protease, serine 5 [Homo sapiens] (SEQ ID NO:74)
8) ~~gi|12248777|dbj|BAB20276.1|~~ BAB20276 **gi|12248777|** (AB016229) type 2 spinesin [Mus musculus] (SEQ ID NO:75)




90 100 110 120
NOV10a SGTLQDEEITLSCSEASAEEALLPALPKTVSFRINSEDFL
NOV10b SGTLQDEEITLSCSEASAEEALLPALPKTVSFRINSEDFL
gi|13540535| SGTLQDEEITLSCSEASAEEALLPALPKTVSFRINSEDFL
gi|13878822| SGTLQEEEMTLNCPGVSCEEELLPSLPKTVSFRINGEDLL
gi|13507652| SGTLQEEEMTLNCPGVSCEEELLPSLPKTVSFRINGEDLL
gi|14770563| SGTLQDEEITLSCSEASAEEALLPALPKTVSFRINSEDFL
gi|12248777| ----------
130 140 150 160
NOV10a LEAQVRDQPRWLLVCHEGWSPALGLQICWSLGHIRLTHHK
NOV10b LEAQVRDQPRWLLVCHEGWSPALGLQICWSLGHIRLTHHK
gi|13540535| LEAQVRDQPRWLLVCHEGWSPALGLQICWSLGHIRLTHHK
gi|13878822| LQVQVRARPDWLLVCHEGWSPALGMHICKSLGHIRLTQHK
gi|13507652| LQVQVRARPDWLLVCHEGWSPALGMHICKSLGHIRLTQHK
gi|14770563| LEAQVRDQPRWLLVCHEGWSPALGLQICWSLGHIRLTHHK
gi|12248777| ----------MHICKSLGHIRLTQHK
170 180 190 200
NOV10a GVNLTDIKLNSSQEFAQLSPRLGGFLEEAWQPSRTTEAVR
NOV10b GVNLTDIKLNSSQEFAQLSPRLGGFLEEAWQP-------R
gi|13540535| GVNLTDIKLNSSQEFAQLSPRLGGFLEEAWQP-------R
gi|13878822| AVNLSDIKLNRSQEFAQLSARPGGLVEEAWKP-------S
gi|13507652| AVNLSDIKLNRSQEFAQLSARPGGLVEEAWKP-------S
gi|14770563| GVNLTDIKLNSSQEFAQLSPRLGGFLEEAWQP-------R
gi|12248777| AVNLSDIKLNRSQEFAQLSARPGGLVEEAWKP-------S
210 220 230 240
NOV10a NNCTSGQVVSLRCSECGARPLASRIVGGQSVAPGRWPWQA
NOV10b NNCTSGQVVSLRCSECGARPLASRIVGGQSVAPGRWPWQA
gi|13540535| NNCTSGQVVSLRCSECGARPLASRIVGGQSVAPGRWPWQA
gi|13878822| ANCPSGRIVSLKCSECGARPLASRIVGGQAVASGRWPWQA
gi|13507652| ANCPSGRIVSLKCSECGARPLASRIVGGQAVASGRWPWQA
gi|14770563| NNCTSGQVVSLRCSECGARPLASRIVGGQSVAPGRWPWQA
gi|12248777| ANCPSGRIVSLKCSECGARPLASRIVGGQAVASGRWPWQA
250 260 270 280
NOV10a SVALGFRHTCGGSVLAPRWVVTAAHCMHSFRLARLSSWRV
NOV10b SVALGFRHTCGGSVLAPRWVVTAAHCMH----------
gi|13540535| SVALGFRHTCGGSVLAPRWVVTAAHCMHSFRLARLSSWRV
gi|13878822| SVMLGSRHTCGASVLAPHWVVTAAHCMYSFRLSRLSSWRV
gi|13507652| SVMLGSRHTCGASVLAPHWVVTAAHCMYSFRLSRLSSWRV
gi|14770563| SVALGFRHTCGGSVLAPRWVVTAAHCMHSFRLARLSSWRV
gi|12248777| SVMLGSRHTCGASVLAPHWVVTAAHCMYSFRLSRLSSWRV
290 300 310 320
NOV10a HAGLVSHSAVRPHQGALVERIIPHPLYSAQNHDYDVALLR
NOV10b ----------SAQNHDYDVALLR
gi|13540535| HAGLVSHSAVRPHQGALVERIIPHPLYSAQNHDYDVALLR
gi|13878822| HAGLVSHGAVRQHQGTMVEKIIPHPLYSAQNHDYDVALLQ
gi|13507652| HAGLVSHGAVRQHQGTMVEKIIPHPLYSAQNHDYDVALLQ
gi|14770563| HAGLVSHSAVRPHQGALVERIIPHPLYSAQNHDYDVALLR
gi|12248777| HAGLVSHGAVRQHQGTMVEKIIPHPLYSAQNHDYDVALLQ
330 340 350 360
NOV10a LQTAPNFSDTVGAVCLPAKEQEFPKGSRCWVSGWGHTHPS



At page 116, please replace Table 10H with the following:

Table 10H Domain Analysis of NOV10

~~gnl|Smart|smart00020,~~ Tryp_SPc, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues. (SEQ ID NO:96)
CD-Length = 230 residues, 100.0% aligned
Score = 266 bits (681), Expect = 2e-72

```
Query:  224  RIVGGQSVAPGRWPWQASVAL-GFRHTCGGSVLAPRWVVTAAHCMHSFRLARLSSWRVHA  282
             |||||      | +||| |+   | || ||||+++||||+|||||++        || ||
Sbjct:  1    RIVGGSEANIGSFPWQVSLQYRGGRHFCGGSLISPRWVLTAAHCVYGSAP---SSIRVRL  57

Query:  283  GLVSHSAVRPHQGALVERIIPHPLYSAQNHDYDVALLRLQTALNFSDTVGAVCLPAKEQH  342
             |    |+    |    | ++| || |+   +| |+|||+|   +  ||||  +|||+   +
Sbjct:  58   GSHDLSSGEETQTVKVSKVIVHPNYNPSTYDNDIALLKLSEPVTLSDTVRPICLPSSGYN  117

Query:  343  FPKGSRCWVSGWGHTHPSHTYSSDMLQDTVVPLLSTQLCNSSCVYSGALTPRMLCAGYLD  402
```

```
                 | |+ | ||||| |  |      | ||+  ||++|   |  +     |+|  ||||| |+
Sbjct:  118  VPAGTTCTVSGWGRTSESSGSLPDTLQEVNVPIVSNATCRRAYSGGPAITDNMLCAGGLE  177

Query:  403  GRADACQGDSGGPLVCPDGDTWRLVGVVSWGR-GCAEPNHPGVYAKVAEFLDWI  455
             |  |||||||||||||| +   | |||+||||  ||| || |||| +|+ +||||
Sbjct:  178  GGKDACQGDSGGPLVC-NDPRWVLVGIVSWGSYGCARPNKPGVYTRVSSYLDWI  230
```

Query: (of SEQ ID NO:27)

Sbjct: (SEQ ID NO:96)

At page 116, please replace Table 10I with the following:

Table 10I. Domain Analysis of NOV10

gnl|Pfam|pfam00089, trypsin, Trypsin. Proteins recognized include all proteins in families S1, S2A, S2B, S2C, and S5 in the classification of peptidases. Also included are proteins that are clearly members, but that lack peptidase activity, such as haptoglobin and protein Z (PRTZ*). (SEQ ID NO:97)
CD-Length = 217 residues, 100.0% aligned
core = 211 bits (538), Expect = 6e-56

```
Query:  225  IVGGQSVAPGRWPWQASVALGFRHTCGGSVLAPRWVVTAAHCMHSFRLARLSSWRVHAGL  284
             ||||+    | +|||  |+ +   | ||||+++  ||+|||||+        ||  ||  |
Sbjct:  1    IVGGREAQAGSFPWQVSLQVSSGHFCGGSLISENWVLTAAHCVSG-----ASSVRVVLGE  55

Query:  285  VSHSAVRPH-QGALVERIIPHPLYSAQNHDYDVALLRLQTALNFSDTVGAVCLPAKEQHF  343
              +         |   |++||  ||  |+      |+|||+|++ +   |||  +|||+
Sbjct:  56   HNLGTTEGTEQKFDVKKIIVHPNYNPDT--NDIALLKLKSPVTLGDTVRPICLPSASSDL  113

Query:  344  PKGSRCWVSGWGHTHPSHTYSSDMLQDTVVPLLSTQLCNSSCVYSGALTPRMLCAGYLDG  403
             | |+ | ||||| |   +  +|| ||+ |||++| + | |+  | | +|  |+|||  | |
Sbjct:  114  PVGTTCSVSGWGRTK--NLGTSDTLQEVVVPIVSRETCRSA--YGGTVTDTMICAGALGG  169

Query:  404  RADACQGDSGGPLVCPDGDTWRLVGVVSWGRGCAEPNHPGVYAKVAEFLDWI  455
             + |||||||||||| ||    |||+|||| |||  |+|||| +|+ +||||
Sbjct:  170  K-DACQGDSGGPLVCSDG---ELVGIVSWGYGCAVGNYPGVYTRVSRYLDWI  217
```

Query: (of SEQ ID NO:27)

Sbjct: (SEQ ID NO:97)